

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Arg	His	Cys	Ser	Ala	Cys	Ser	Thr	Thr	Ser	Gly	Arg	Gly	Ala	Pro	Ala
1															15

Ser	Trp	Ala	Pro	Leu	Cys	Trp	Ala	Trp	Thr	Ile	Ser	Thr	Gly	Pro	Gly
															30
20															

Ala	Pro	Ser	Cys	Cys	Val	Cys	Gly	Pro	Arg	Thr	Arg	Arg	Leu	Ser	Cys
															45
35															

Thr	Leu	Ser	Arg	Trp	Met
					50

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Arg	Ala	Arg	Thr	Thr	Pro	Ser	Pro	Arg	Thr	Gly	Ser	Arg	Arg	Ser	Ser
1															15

Pro	Ala	Ser	Ser	Asn	Pro	Arg	Thr	Arg	Thr	Ala	Cys	Val	Gly	Met	Pro
															30
20															

Trp	Ser	Arg	Arg	Pro	Pro	Met	Gly	Thr	Ser	Ala	Arg	Pro	Ser	Arg	Ala
															45
35															

Thr	Ser	Leu	Pro
			50

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Gln	Thr	Ser	Ser	Arg	Thr	Cys	Asp	Ser	Ser	Trp	Leu	Thr	Cys	Arg	Xaa
1															15
5															
10															
Thr Ala Arg															

(2) INFORMATION FOR SEQ ID NO:305:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

Gly	Met	Pro	Ser	Ser	Ser	Ser	Arg	Ala	Pro	Pro
1										
5										
10										

(2) INFORMATION FOR SEQ ID NO:306:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Met	Arg	Pro	Ala	Val	Ala	Ser	Ser	Thr	Ser	Ser	Tyr	Ala	Ser	Cys	Ala
1															15
5															
10															
Thr	Thr	Pro	Cys	Ala	Ser	Gly	Ala	Ser	Pro	Thr	Ser	Ser	Ala	Arg	Gly
															30
20															
25															
Ser	Arg	Arg	Ala	Pro	Ser	Ser	Pro	Arg	Cys	Ser	Ala	Ala	Cys	Ala	Thr
															45
35															
40															
Ala	Thr	Trp	Arg	Thr	Ser	Cys	Leu	Arg	Gly	Phe	Gly	Thr	Gly	Cys	
															60
50															
55															
Ser	Cys	Val	Trp	Trp	Met	Ile	Ser	Cys	Trp						
65															
70															

(2) INFORMATION FOR SEQ ID NO:307:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

His	Leu	Thr	Ser	Pro	Thr	Arg	Lys	Pro	Ser	Ser	Gly	Pro	Trp	Ser	Glu
1				5					10				15		

Val	Ser	Leu	Ser	Met	Ala	Ala	Trp
				20			

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Thr	Cys	Gly	Arg	Gln	Trp
1			5		

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

Lys	Thr	Arg	Pro	Trp	Val	Ala	Arg	Leu	Leu	Phe	Arg	Cys	Arg	Pro	Thr
1				5				10				15			

Ala	Tyr	Ser	Pro	Gly	Ala	Ala	Cys	Cys	Trp	Ile	Pro	Gly	Pro	Trp	Arg
					20			25				30			

Cys	Arg	Ala	Thr	Thr	Pro	Ala	Met	Pro	Gly	Pro	Pro	Ser	Glu	Pro	Val
						35		40				45			

Ser	Pro	Ser	Thr	Ala	Ala	Ser	Arg	Leu	Gly	Gly	Thr	Cys	Val	Ala	Asn
				50			55				60				

Ser	Leu	Gly	Ser	Cys	Gly
65				70	

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Ser	Val	Thr	Ala	Cys
1				5

10

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Thr	Ala	Ser	Arg	Arg
1				5

10

15

Arg	Arg	Thr	Gly	Phe
20				25

30

Lys	Phe	Gly	Arg	Thr	Pro
35					40

45

Pro	Pro	Ser	Ala	Thr	Pro
50					55

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Lys	Pro	Arg	Thr	Gln	Gly	Cys	Arg	Trp	Gly
1						5			10

15

Leu Cys Pro Pro Arg Pro Cys Ser Gly Cys Ala Thr Lys His Ser Cys
 20 25 30
 Ser Ser

(2) INFORMATION FOR SEQ ID NO:313:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

Leu Asp Thr Val Ser Pro Thr Cys His Ser Trp Gly His Ser Gly Gln
 1 5 10 15
 Pro Arg Arg Ser
 20

(2) INFORMATION FOR SEQ ID NO:314:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Val Gly Ser Ser Arg Gly Arg Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:315:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

Leu Pro Trp Arg Pro Gln Pro Thr Arg His Cys Pro Gln Thr Ser Arg
 1 5 10 15
 Pro Ser Trp Thr Asp Gly His Pro Pro Thr Ala Arg Pro Arg Ala Asp
 20 25 30

Thr Ser Ser Pro Val Thr Pro Gly Ser Thr Ser Gln Gly Gly Arg Gly		
35	40	45
Gly Pro His Pro Gly Pro His Arg Trp Glu Ser Glu Ala		
50	55	60

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

Val Ser Val Trp Pro Arg Pro Ala Cys Pro Ala Glu Gly		
1	5	10

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Gly Leu Ser Glu Cys Pro Ala Lys Gly	
1	5

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Val Ser Ser Thr Pro Ala Val Phe Thr Ser Pro Gln Ala Gly Ala Arg			
1	5	10	15

Leu His Pro Arg Ala Ser Phe Ser Ser Pro Gly Ala Arg Leu Pro Leu		
20	25	30

Pro Thr

(2) INFORMATION FOR SEQ ID NO:319:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- ii) MOLECULE TYPE: peptide
- x) SEQUENCE DESCRIPTION: SEQ ID NO:319:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

Ser Ile Pro Arg Phe Ala Ile Val His Pro Ser Pro Cys Pro Pro Leu
1 5 10 15

Pro Ser Thr Pro Thr Ile Gln Val Glu Thr Leu Arg Arg Thr Leu Gly
20 25 30

Ala Leu Gly Ile Trp Ser Asp Gln Arg Cys Ala Leu Tyr Thr Gly Glu
35 40 45

Asp Pro Ala Pro Gly Trp Gly Ser Leu Trp Val Lys Leu Gly Gly Gly
50 55 . 60

Ala Val Gly Val Lys Tyr
65 70

(2) INFORMATION FOR SEQ ID NO:320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

(2) INFORMATION FOR SEO ID NO: 321:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu Ala Pro Ala Thr
1 5 10 15

Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu
 20 25 30

Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg
 35 40 45

Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala
 50 55 60

Phe Arg Ala Xaa Val Ala Xaa Cys Xaa Val Cys Val Pro Trp Xaa Xaa
 65 70 75 80

Xaa Xaa Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Xaa
 85 90 95

Xaa Leu Val Ala Arg Val Leu Xaa Xaa Leu Cys Xaa Arg Gly Ala Xaa
 100 105 110

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 115 120 125

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 130 135 140

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 145 150 155 160

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Xaa
 165 170 175

Phe Val Leu Val Xaa Pro Ser Cys Ala Tyr Xaa Val Cys Gly Pro Pro
 180 185 190

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 195 200 205

Xaa Gly Pro Glu Xaa Val Trp Asp Pro Thr Gly Leu Glu Pro
 210 215 220

(2) INFORMATION FOR SEQ ID NO:322:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Arg Gln Gly Gly Arg Gly Pro Pro Gly Leu Pro Ala Pro Gly Ala Arg
 1 5 10 15

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 20 25 30

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 35 40 45

Ser Trp Ala His Pro Gly Arg Thr Pro Gly Pro Ser Asp Arg Gly Phe
 50 55 60

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 65 70 75 80

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 85 90 95

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Gly Thr
 100 105 110

Arg Leu Val Pro Arg Cys Thr Pro Arg Pro Ser Thr Ser Ser Thr Pro
 115 120 125

Gln Ala Thr Xaa Thr Leu Arg Pro Ser Phe Leu Leu Asn Ile Ser Glu
 130 135 140

Ala Gln Pro Asp Trp Arg Ser Gly Gly Ser Trp Arg Xaa Ser Phe Trp
 145 150 155 160

Phe Gln Ala Leu Asp Ala Arg Ile Pro Arg Arg Leu Pro Arg Leu Pro
 165 170 175

Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn
 180 185 190

His Ala Gln Cys Pro Tyr Gly Val Phe Leu Lys Thr His Cys Pro Leu
 195 200 205

Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro
 210 215 220

Gln Gly Ser Val Ala Ala Pro Glu Glu Glu His Arg Pro Pro Ser
 225 230 235 240

Pro Gly Ala Ala Ala Pro Pro Ala Gln Gln Pro Leu Ala Gly Val Arg
 245 250 255

Leu Arg Ala Gly Leu Pro Ala Pro Ala Gly Ala Pro Arg Pro Leu Gly
 260 265 270

Leu Gln Ala Gln Arg Thr Pro Leu Pro Gln Glu His Gln Glu Val His
 275 280 285

Leu Pro Gly Glu Ala Cys Gln Ala Leu Ala Ala Gly Ala Asp Val Glu
 290 295 300

Asp Glu Arg Ala Gly Leu Arg Leu Ala Ala Gln Glu Pro Arg Gly Trp
 305 310 315 320

Leu Cys Ser Gly Arg Arg Ala Pro Ser Ala
 325 330

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Gly	Asp	Pro	Gly	Gln	Val	Pro	Ala	Leu	Ala	Asp	Glu	Cys	Val	Arg	Arg
1					5					10				15	

Arg	Ala	Ala	Gln	Val	Phe	Leu	Leu	Cys	His	Gly	Asp	His	Val	Ser	Lys
					20				25				30		

Glu	Gln	Ala	Leu	Phe	Leu	Pro	Glu	Glu	Cys	Leu	Glu	Gln	Val	Ala	Lys
						35		40				45			

His	Trp	Asn	Gln	Thr	Ala	Leu	Glu	Glu	Gly	Ala	Ala	Gly	Ala	Val	
					50		55				60				

Gly	Ser	Arg	Gly	Gln	Ala	Ala	Ser	Gly	Ser	Gln	Ala	Arg	Pro	Ala	Asp
					65		70		75			80			

Val	Gln	Thr	Pro	Leu	His	Pro	Gln	Ala							
					85										

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Arg	Ala	Ala	Ala	Asp	Cys	Glu	His	Gly	Leu	Arg	Arg	Gly	Ser	Gln	Asn
1					5				10				15		

Val	Pro	Gln	Arg	Lys	Glu	Gly	Arg	Ala	Ser	His	Leu	Glu	Gly	Glu	Gly
					20			25			30				

Thr	Val	Gln	Arg	Ala	Gln	Leu	Arg	Ala	Gly	Ala	Ala	Pro	Arg	Pro	Pro
						35		40			45				

Gly	Arg	Leu	Cys	Ala	Gly	Pro	Gly	Arg	Tyr	Pro	Gln	Gly	Leu	Ala	His
					50		55				60				

Leu	Arg	Ala	Ala	Cys	Ala	Gly	Pro	Gly	Pro	Ala	Ala				
					65		70		75						

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Ala Val Leu Cys Gln Gly Gly Cys Asp Gly Arg Val Arg His His Pro
1 5 10 15

Pro Gly Gln Ala His Gly Gly His Arg Gln His His Gln Thr Pro Glu
20 25 . 30

His Val Leu Arg Ala Ser Val Cys Arg Gly Pro Glu Gly Arg Pro Trp
35 40 45

Ala Arg Pro Gln Gly Leu Gln Glu Pro Arg Leu Tyr Leu Asp Arg Pro
50 55 60

Pro Ala Val His Ala Thr Val Arg Gly Ser Pro Ala Gly Xaa Gln Pro
65 70 75 80

Ala Glu Gly Cys Arg Arg His Arg Ala Glu Leu Leu Pro Glu
85 90

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

Gly Gln Gln Trp Pro Leu Arg Arg Leu Pro Thr Leu His Val Pro Pro
1 5 . . . 10 . . . 15

Arg Arg Ala His Gln Gly Gln Val Leu Arg Pro Val Pro Gly Asp Pro
20 25 30

Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg
35 40 45

His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro
50 55 60

Ala Phe Gly Gly
65

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

Phe	Leu	Val	Gly	Asp	Thr	Ser	Pro	His	Pro	Arg	Glu	Asn	Leu	Pro	Gln
1															15
Asp Pro Gly Pro Arg Cys Pro															
20															

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Val	Trp	Leu	Arg	Gly	Glu	Leu	Ala	Glu	Asp	Ser	Gly	Glu	Leu	Pro	Cys
1															15
Arg Arg Arg Gly Pro Gly Trp His Gly Phe Cys Ser Asp Ala Gly Pro															
20 25 30															
Arg Pro Ile Pro Leu Val Arg Pro Ala Ala Gly Tyr Pro Asp Pro Gly															
35 40 45															
Gly Ala Glu Arg Leu Leu Gln Leu Cys Pro Asp Leu His Gln Ser Gln															
50 55 60															
Ser His Leu Gln Pro Arg Leu Gln Gly Trp Glu Glu His Ala Ser Gln															
65 70 75 80															
Thr Leu Trp Gly Leu Ala Ala Glu Val Ser Gln Pro Val Ser Gly Phe															
85 90 95															
Ala Gly Glu Gln Pro Pro Asp Gly Val His Gln His Leu Gln Asp Pro															
100 105 110															
Pro Ala Ala Gly Val Gln Val Ser Arg Met Cys Ala Ala Ala Pro Ile															
115 120 125															
Ser Ser Ala Ser Leu Glu Glu Pro His Ile Phe Pro Ala Arg His Leu															
130 135 140															

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

His	Gly	Leu	Pro	Leu	Leu	Leu	His	Pro	Glu	Ser	Gln	Glu	Arg	Arg	Asp
1															15

Val	Ala	Gly	Gly	Gln	Gly	Arg	Arg	Arg	Pro	Ser	Ala	Leu	Arg	Gly	Arg
															30
20															

Ala	Val	Ala	Val	Pro	Pro	Ser	Ile	Pro	Ala	Gln	Ala	Asp	Ser	Thr	Pro
															45
35															

Cys	His	Leu	Arg	Ala	Thr	Pro	Gly	Val	Thr	Gln	Asp	Ser	Pro	Asp	Ala
															60
50															

Ala	Glu	Ser	Glu	Ala	Pro	Gly	Asp	Asp	Ala	Asp	Cys	Pro	Gly	Gly	Arg
															80
65															

Ser	Gln	Pro	Gly	Thr	Ala	Leu	Arg	Leu	Gln	Asp	His	Pro	Gly	Leu	Met
															95
85															

Ala	Thr	Arg	Pro	Gln	Pro	Gly	Arg	Glu	Gln	Thr	Pro	Ala	Ala	Leu	Ser
															110
100															

Arg	Arg	Ala	Leu	Arg	Pro	Arg	Glu	Gly	Gly	Ala	Ala	His	Thr	Gln	Ala
															125
115															

Arg	Thr	Ala	Gly	Ser	Leu	Arg	Pro	Glu							
															135
130															

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Val	Phe	Gly	Arg	Gly	Leu	His	Val	Arg	Leu	Lys	Ala	Glu	Cys	Pro	Ala
1															15
5															

Glu Ala

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Ala	Ser	Val	Gln	Pro	Arg	Ala	Glu	Cys	Pro	Ala	His	Leu	Pro	Ser	Ser
1															15

Leu	Pro	His	Arg	Leu	Ala	Leu	Gly	Ser	Thr	Pro	Gly	Pro	Ala	Phe	Pro
															30
				20				25							

His	Gln	Glu	Pro	Gly	Phe	His	Ser	Pro	His	Arg	Asn	Ser	Pro	Ser	Pro
															45
							35		40						

Asp	Ser	Pro	Leu	Phe	Thr	Pro	Arg	Pro	Ala	Leu	Leu	Cys	Leu	Pro	Pro
															60
							50		55						

Pro	Pro	Ser	Arg	Trp	Arg	Pro									
															70
				65											

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Glu	Gly	Pro	Trp	Glu	Leu	Trp	Glu	Phe	Gly	Val	Thr	Lys	Gly	Val	Pro
1															15
					5										

Cys	Thr	Gln	Ala	Arg	Thr	Leu	His	Leu	Asp	Gly	Gly	Pro	Cys	Gly	Ser
															30
					20			25							

Asn	Trp	Gly	Glu	Val	Leu	Trp	Glu								
							35		40						

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Asn	Thr	Glu	Tyr	Met	Ser	Phe	Ser	Val	Leu	Lys	Lys	Lys	Lys	Lys
1									10					15
Lys Lys														

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Ser	Ala	Ala	Ser	Cys	Cys	Ala	Arg	Gly	Lys	Pro	Trp	Pro	Arg	Pro	Pro
1									10						15

Pro	Arg	Cys	Arg	Ala	Leu	Pro	Ala	Ala	Glu	Pro	Cys	Ala	Pro	Cys	Cys
									25					30	

Ala	Ala	Thr	Thr	Ala	Arg	Cys	Cys	Arg	Trp	Pro	Arg	Ser	Cys	Gly	Ala
									40					45	

Trp	Gly	Pro	Arg	Ala	Gly	Gly	Trp	Cys	Ser	Ala	Gly	Thr	Arg	Arg	Leu
									55					60	

Ser	Ala	Arg	Trp	Trp	Pro	Xaa	Ala	Trp	Cys	Ala	Cys	Pro	Gly	Xaa	Xaa
									70					75	80

Gly	Xaa	Pro	Pro	Pro	Pro	Pro	Ser	Ala	Arg	Cys	Pro	Ala			
									85				90		

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

Xaa	Xaa	Trp	Trp	Pro	Glu	Cys	Cys	Xaa	Xaa	Cys	Ala	Xaa	Ala	Ala	Arg
1									5					10	15

Xaa	Thr	Cys	Trp	Pro	Ser	Ala	Ser	Arg	Cys	Trp	Thr	Gly	Pro	Ala	Gly
									20					25	30

Ala Pro Pro Arg Pro Ser Pro Pro Ala Cys Ala Ala Thr Cys Pro Thr
 35 40 45

Arg

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

Pro Thr His Cys Gly Gly Ala Gly Arg Gly Gly Cys Cys Cys Ala Ala
 1 5 10 15

Trp Ala Thr Thr Cys Trp Phe Thr Cys Trp His Ala Ala Arg Xaa Leu
 20 25 30

Cys Trp Trp Xaa Pro Ala Ala Pro Thr Xaa Cys Ala Gly Arg Arg Cys
 35 40 45

Thr Ser Ser Ala Leu Xaa Leu Arg Pro Gly Pro Arg His Thr Leu Xaa
 50 55 60

Asp Pro Xaa Ala Ser Gly Ile Gln Arg Ala Trp Asn His Ser Val Arg
 65 70 75 80

Glu Ala Gly Val Pro Leu Gly Cys Gln Pro Arg Val Arg Gly Gly Ala
 85 90 95

Gly Ala Val Pro Ala Glu Val Cys Arg Cys Pro Arg Gly Pro Gly Val
 100 105 110

Ala Leu Pro Leu Ser Arg Ser Gly Arg Pro Leu Gly Arg Gly Pro Gly
 115 120 125

Pro Thr Arg Ala Gly Arg Leu Asp Arg Val Thr Val Val Ser Val Trp
 130 135 140

Cys His Leu Pro Asp Pro Pro Lys Lys Pro Pro Leu Trp Arg Val Arg
 145 150 155 160

Ser Leu Ala Arg Ala Thr Pro Thr His Pro Trp Ala Ala Ser Thr Thr
 165 170 175

Arg Ala Pro His Pro His Arg Gly His His Val Leu Gly His Ala Leu
 180 185 190

Ser Pro Gly Val Arg Arg Asp Gln Ala Leu Pro Leu Leu Leu Arg Arg
 195 200 205

Gln Xaa His Cys Xaa Pro Pro Ser Tyr Ser Ile Tyr Leu Arg Pro Ser
 210 215 220

Leu Thr Gly Val Arg Glu Val Arg Gly Asp Xaa Leu Ser Gly Ser Arg
 225 230 235 240
 Pro Trp Met Pro Gly Phe Pro Ala Gly Cys Pro Ala Cys Pro Ser Xaa
 245 250 255
 Thr Gly Lys Cys Gly Pro Cys Phe Trp Ser Cys Leu Gly Thr Thr Arg
 260 265 270
 Ser Ala Pro Thr Gly Cys Ser Ser Arg Arg Thr Ala Arg Cys Glu Leu
 275 280 285
 Arg Ser Pro Gln Gln Pro Val Ser Val Pro Gly Arg Ser Pro Arg Ala
 290 295 300
 Leu Trp Arg Pro Pro Arg Arg Asn Thr Asp Pro Arg Arg Leu Val
 305 310 315 320
 Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val
 325 330 335
 Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg
 340 345 350
 His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu
 355 360 365
 Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser
 370 375 380
 Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val
 385 390 395 400
 Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu
 405 410 415
 His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe
 420 425 430
 Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg
 435 440 445
 Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu
 450 455 460
 Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His
 465 470 475 480
 Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro
 485 490 495
 Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly
 500 505 510
 Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
 515 520 525
 Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro
 530 535 540

Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala
 545 550 555 560
 Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu
 565 570 575
 Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro
 580 585 590
 Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn
 595 600 605
 Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly
 610 615 620
 His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu
 625 630 635 640
 Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Xaa Asn Ser Pro
 645 650 655
 Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala
 660 665 670
 Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala
 675 680 685
 Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln
 690 695 700
 Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met
 705 710 715 720
 Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Arg
 725 730 735
 Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys
 740 745 750
 Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val
 755 760 765
 Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala
 770 775 780
 Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro
 785 790 795 800
 Trp Cys Gly Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp
 805 810 815
 Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn
 820 825 830
 Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val
 835 840 845
 Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser
 850 855 860

Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala
 865 870 875 880
 Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val
 885 890 895
 Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser
 900 905 910
 Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly
 915 920 925
 Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu
 930 935 940
 Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr
 945 950 955 960
 Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg
 965 970 975
 Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Asn Pro
 980 985 990
 Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 995 1000

(2) INFORMATION FOR SEQ ID NO:337:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

Trp Pro Pro Ala His Ser Gln Ala Glu Ser Arg His Gln Gln Pro Cys
 1 5 10 15
 His Ala Gly Leu Tyr Val Pro Gly Arg Glu Gly Arg Pro Thr Pro Arg
 20 25 30
 Pro Ala Pro Leu Gly Val
 35

(2) INFORMATION FOR SEQ ID NO:338:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

Gly	Leu	Ser	Glu	Cys	Leu	Ala	Glu	Ala	Cys	Met	Ser	Gly
1				5						10		

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

Arg	Leu	Ser	Val	Arg	Leu	Arg	Pro	Glu	Arg	Val	Ser	Ser	Gln	Gly	Leu
1				5					10				15		

Ser	Val	Gln	His	Thr	Cys	Arg	Leu	His	Phe	Pro	Thr	Gly	Trp	Arg	Ser
				20				25				30			

Ala	Pro	Pro	Gln	Gly	Gln	Leu	Phe	Leu	Thr	Arg	Ser	Pro	Ala	Ser	Thr
					35			40			45				

Pro	His	Ile	Gly	Ile	Val	His	Pro	Gln	Ile	Arg	His	Cys	Ser	Pro	Leu
		50				55				60					

Ala	Leu	Pro	Ser	Phe	Ala	Phe	His	Pro	His	His	Pro	Gly	Gly	Asp	Pro
65				70					75			80			

Glu	Lys	Asp	Pro	Gly	Ser	Ser	Gly	Asn	Leu	Glu
					85			90		

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Pro	Lys	Val	Cys	Pro	Val	His	Arg	Arg	Gly	Pro	Cys	Thr	Trp	Met	Gly
1				5					10			15			

Val	Pro	Val	Gly	Gln	Ile	Gly	Gly	Arg	Cys	Cys	Gly	Ser	Lys	Ile	Leu
					20			25			30				

Asn Ile

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Val Phe Gln Phe
1

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Lys Lys Lys Lys Lys Lys Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4037 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 56..3454
- (D) OTHER INFORMATION: /note= "refined sequence of hTRT cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC CCGCG ATG	58
Met	
1	

CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC	106
Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His	
5 10 15	

TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG GGG CCC Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro 20 25 30	154
CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala 35 40 45	202
CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro 50 55 60 65	250
CCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val 70 75 80	298
GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu 85 90 95	346
GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu 100 105 110	394
GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp 115 120 125	442
GCA CTG CGG GGG AGC GGG GCG TGG GGG CTG CTG CTG CGC CGC GTG GGC Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly 130 135 140 145	490
GAC GAC GTG CTG GTT CAC CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu 150 155 160	538
GTG GCT CCC AGC TGC GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln 165 170 175	586
CTC GGC GCT GCC ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro His Ala Ser Gly Pro 180 185 190	634
CGA AGG CGT CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu 195 200 205	682
GCC GGG GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly 210 215 220 225	730
GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly 230 235 240	778
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG GCC Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala 245 250 255	826

CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT GTG GTG His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val 260 265 270	874
TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG GGT GCG CTC Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu 275 280 285	922
TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC CAG CAC CAC GCG Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala 290 295 300 305	970
GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC TGG GAC ACG CCT TGT Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys 310 315 320	1018
CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC CTC TAC TCC TCA GGC GAC Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp 325 330 335	1066
AAG GAG CAG CTG CGG CCC TCC TTC CTA CTC AGC TCT CTG AGG CCC AGC Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser 340 345 350	1114
CTG ACT GGC GCT CGG AGG CTC GTG GAG ACC ATC TTT CTG GGT TCC AGG Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg 355 360 365	1162
CCC TGG ATG CCA GGG ACT CCC CGC AGG TTG CCC CGC CTG CCC CAG CGC Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg 370 375 380 385	1210
TAC TGG CAA ATG CGG CCC CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala 390 395 400	1258
CAG TGC CCC TAC GGG GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala 405 410 415	1306
GCG GTC ACC CCA GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly 420 425 430	1354
TCT GTG GCG GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val 435 440 445	1402
CAG CTG CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val 450 455 460 465	1450
CGG GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg 470 475 480	1498
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC CTG His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu 485 490 495	1546

GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG ATG AGC Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser 500 505 510	1594
GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT GGC TGT GTT Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val 515 520 525	1642
CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG GCC AAG TTC CTG Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu 530 535 540 545	1690
CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG CTC AGG TCT TTC TTT His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe 550 555 560	1738
TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG CTC TTT TTC TAC CGG Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe Tyr Arg 565 570 575	1786
CCG AGT GTC TGG AGC AAG TTG CAA AGC ATT GGA ATC AGA CAG CAC TTG Pro Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu 580 585 590	1834
AAG AGG GTG CAG CTG CGG GAG CTG TCG GAA GCA GAG GTC AGG CAG CAT Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His 595 600 605	1882
CGG GAA GCC AGG CCC GCC CTG CTG ACG TCC AGA CTC CGC TTC ATC CCC Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro 610 615 620 625	1930
AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly 630 635 640	1978
GCC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg 645 650 655	2026
GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro 660 665 670	2074
GCC CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala 675 680 685	2122
TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu 690 695 700 705	2170
CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro 710 715 720	2218
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn 725 730 735	2266

ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC CAT GGG Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly 740 745 750	2314
CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG ACA GAC CTC His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu 755 760 765	2362
CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG GAG ACC AGC CCG Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro 770 775 780 785	2410
CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC TCC CTG AAT GAG GCC Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala 790 795 800	2458
AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC TTC ATG TGC CAC CAC GCC Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala 805 810 815	2506
GTG CGC ATC AGG GGC AAG TCC TAC GTC CAG TGC CAG GGG ATC CCG CAG Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln 820 825 830	2554
GCC TCC ATC CTC TCC ACG CTG CTC TGC AGC CTG TGC TAC GGC GAC ATG Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met 835 840 845	2602
GAG AAC AAG CTG TTT GCG GGG ATT CGG CGG GAC GGG CTG CTC CTG CGT Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg 850 855 860 865	2650
TTC GTG GAT GAT TTC TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys 870 875 880	2698
ACC TTC CTC AGG ACC CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val 885 890 895	2746
GTG AAC TTG CGG AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala 900 905 910	2794
CTG GGT GGC ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro 915 920 925	2842
TGG TGC GGC CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp 930 935 940 945	2890
TAC TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Val Thr Phe Asn 950 955 960	2938
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val 965 970 975	2986

TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser 980 985 990	3034
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG GCG Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Gln Ala 995 1000 1005	3082
TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG CAA GTT Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val 1010 1015 1020 1025	3130
TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC TCT GAC ACG GCC TCC Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser 1030 1035 1040	3178
CTC TGC TAC TCC ATC CTG AAA GCA GGG ATG TCG CTG GGG Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly 1045 1050 1055	3226
GCC AAG GGC GCC GGC CCT CTG CCC TCC GAG GCC GTG CAG TGG CTG Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu 1060 1065 1070	3274
TGC CAC CAA GCA TTC CTG CTC AAG CTG ACT CGA CAC CGT GTC ACC TAC Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr 1075 1080 1085	3322
GTC CCA CTC CTG GGG TCA CTC AGG ACA GCC CAG ACG CAG CTG AGT CGG Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg 1090 1095 1100 1105	3370
AAC CTC CCG GGG ACG ACG CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Asn Pro 1110 1115 1120	3418
GCA CTG CCC TCA GAC TTC AAG ACC ATC CTG GAC TGATGGCCAC CGGCCACAG Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp 1125 1130	3471
CCAGGCCGAG AGCAGACACC AGCAGCCCTG TCACGCCGGG CTCTACGTCC CAGGGAGGGA	3531
GGGGCGGCC ACACCCAGGC CCGCACCGCT GGGAGTCTGA GGCTTGAGTG AGTGTGGC	3591
CGAGGCCCTGC ATGTCCGGCT GAAGGCTGAG TGTCCGGCTG AGGCCTGAGC GAGTGTCCAG	3651
CCAAGGGCTG AGTGTCCAGC ACACCTGCCG TCTTCACTTC CCCACAGGCT GGCGCTCGGC	3711
TCCACCCAG GGCCAGCTTT TCYTCACCAG GAGCCCGGCT TCCACTCCCC ACATAGGAAT	3771
AGTCCATCCC CAGATTCGCC ATTGTTCACCC CYTCGCCCTG CCYTCCTTTG CCTTCCACCC	3831
CCACCATCCA GGTGGAGACC CTGAGAAGGA CCCTGGGAGC TCTGGGAATT TGGAGTGACC	3891
AAAGGTGTGC CCTGTACACA GGCGAGGACC CTGCACCTGG ATGGGGTCC CTGTGGGTCA	3951
AATTGGGGGG AGGTGCTGTG GGAGTAAAAT ACTGAATATA TGAGTTTTC AGTTTGRAA	4011
AAAAAAAAAA AAAAAAAAAA AAAAAA	4037

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Met	Pro	Arg	Ala	Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser
1															

5

10

15

His	Tyr	Arg	Glu	Va	L	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly

20

25

30

Pro	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg

35

40

45

Ala	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro

50

55

60

Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu

65

70

75

80

Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val

85

90

95

Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Pro	Pro	

100

105

110

Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr

115

120

125

)	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Arg	Arg	Val

130

135

140

Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val

145

150

155

160

Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr

165

170

175

Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly

180

185

190

Pro	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg

195

200

205

Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg

210

215

220

Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg

225

230

235

240

Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp

245

250

255

Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val

260

265

270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Pro Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800
 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815
 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925
 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940
 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Val Thr Phe
 945 950 955 960
 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975
 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Gln
 995 1000 1005
 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
 1010 1015 1020
 Val Trp Lys Asn Pro Thr Phe Leu Arg Val Ile Ser Asp Thr Ala
 1025 1030 1035 1040
 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
 1045 1050 1055
 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
 1060 1065 1070
 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
 1075 1080 1085
 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
 1090 1095 1100
 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
 1105 1110 1115 1120
 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1125 1130

(2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1
 - (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 Ala, Leu, Ile, Val, Pro, Phe, Trp
 or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

Xaa Xaa Asp Asp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Xaa Xaa Asp Asp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Trp Xaa Gly Xaa Ser Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
 $\text{/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"}$

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
 $\text{/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"}$

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Xaa Leu Gly Xaa Xaa Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7..8
- (D) OTHER INFORMATION: /product= "OTHER"
 $\text{/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"}$

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10..11
- (D) OTHER INFORMATION: /product= "OTHER"
 $\text{/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"}$

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid, Gly,
 Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid, Gly,
 Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 23
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid, Gly,
 Ser, Thr, Tyr, Cys, Asn or Gln"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Trp	Leu	Xaa	Tyr	Xaa	Phe	Phe	Thr							
1														15

Glu	Xaa	Tyr	Xaa	Arg	Lys	Xaa	Xaa							
														30
	20								25					

Trp

(x) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7..8
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 Ala, Leu, Ile, Val, Pro, Phe, Trp
 or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 10..11
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 Ala, Leu, Ile, Val, Pro, Phe, Trp
 or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 12
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Gln or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 13
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid, Gly,
 Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 21
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid, Gly,
 Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 25
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid, Gly,
 Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 28..29
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Phe or Tyr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 31
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Trp	Xaa	Phe	Phe	Tyr									
1													15

Xaa	Thr	Glu	Xaa	Arg	Xaa	Xaa							
			20								30		

Xaa Trp

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7..8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10..11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 25
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29..30
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Trp	Xaa	Phe	Phe	Tyr									
1													15
Xaa	Thr	Glu	Xaa	Arg	Xaa								
												30	
Xaa	Xaa	Trp											
		35											

(2) INFORMATION FOR SEQ ID NO:352:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

Trp	Xaa	Phe	Phe	Tyr									
1													15
Xaa	Thr	Glu	Xaa	Arg	Xaa	Xaa							
											30		
Xaa	Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ile					
							40						

(2) INFORMATION FOR SEQ ID NO:353:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

Trp Xaa Phe Phe Tyr			
1	5	10	15
Xaa Thr Glu Xaa Arg Xaa			
20		25	30
Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Ile			
35		40	

(2) INFORMATION FOR SEQ ID NO:354:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Glu Xaa Xaa Val Xaa			
1	5		

(2) INFORMATION FOR SEQ ID NO:355:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Xaa Xaa Xaa Arg Xaa Xaa Pro Lys Xaa Xaa Xaa			
1	5	10	

(2) INFORMATION FOR SEQ ID NO:356:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

Xaa Arg Xaa Ile Xaa			
1	5		

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Tyr Asp Xaa
1 5 10 15

Xaa

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

Tyr Xaa Xaa Xaa Xaa Gly Xaa Xaa Gln Gly Xaa Xaa Xaa Ser Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa
20

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

Xaa Xaa Xaa Xaa Xaa Xaa Asp Asp Xaa Leu Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

Phe Phe Tyr Xaa Thr Glu
1 5

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

Phe Phe Tyr Val Thr Glu
1 5

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

TTYTTYTAYG TNACNGA

17

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

TCNGTNACRT ARAARAA

17

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Arg	Phe	Ile	Pro	Lys	Pro
1				5	

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

AGCTTATTC CNAARCC

17

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GGYTTNGGDA TRAAC

16

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

Ala Tyr Asp Thr Ile
1 5

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

GCNTAYGAYA CNAT

14

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

TANGTRTCRT ANGC

14

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Gly Ile Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

GGNATHCCNC ARGG

14

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

SWNCCYTGNG GDATNCC

17

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

Leu Val Asp Asp Phe Leu
1 5

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

YTNNGTNGAYG AYTYYYT

17

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Asp	Asp	Phe	Leu	Leu	Val	Thr
1						5

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

GTNACNARNA RRAARTCRTC

20

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCPl.1 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

GTGAAGGCAC TGTTCAGCG

19

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.15 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

CGCGTGGGTG AGGTGAGGTG

20

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.14 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

CTGTGCTGGG CCTGGACGAT A

21

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "billTCP6 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

AGCTTGTCTT CCATGTCGCC GTAG

24

(2) INFORMATION FOR SEQ ID NO:381:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

GTGGATGATT TCTTGTTGG

19

(2) INFORMATION FOR SEQ ID NO:382:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

CTGGACACTC AGCCCTTGG

19

(2) INFORMATION FOR SEQ ID NO:383:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.5 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

GGCAGGTGTG CTGGACACT

19

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.6 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

TTTGATGATG CTGGCGATG

19

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.7 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

GGGGCTCGTC TTCTACAGG

19

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.8 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

CAGCAGGAGG ATCTTGTAG

19

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.9 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

TGACCCCAGG AGTGGCACG

19

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.10 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

TCAAGCTGAC TCGACACCG

19

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "TCP1.11 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

CGCGGTGACA GGGCTGC

17

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "TCP1.12 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GCTGAAGGCT GAGTGTC

18

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.13 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

TAGTCCATGT TCACAATCG

19

(2) INFORMATION FOR SEQ ID NO:392:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.16 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

TTTCCGTGTT GAGTGTTTC

19

(2) INFORMATION FOR SEQ ID NO:393:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "TCP1.17 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

GTCACCGTGT TGGGCAGG

18

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "TCP1.19 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GCTACCTGCC CAACACGG

18

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "TCP1.20 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

GCGCGAAGAA CGTGCTGG

18

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.21 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

CACTGCTCCT TGTCGCCCTG

19

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.22 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

TTCCCAAGGA CTTTGTGCG

19

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.24 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

TGTTCCCTCAA GACGCACTG

19

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.25 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

TACTGCGTGC GTCGGTATG

19

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.26 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

GGTCTTGCAG CTGAAGTGT

19

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.27 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

TGGTTCACCT GCTGGCACG

19

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.28 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

GTGGTTTCTG TGTGGTGTC

19

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.29 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

GACACCACAC AGAAACCAC

19

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.30 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

GTGCCAGCAG GTGAACCAG

19

(2) INFORMATION FOR SEQ ID NO:405:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.32B primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

GCAGTGCCTC TTGAGGAGC

19

(2) INFORMATION FOR SEQ ID NO:406:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.33 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

TGGAACCATA GCGTCAGGGA G

21

(2) INFORMATION FOR SEQ ID NO:407:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.34 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

GGCCTCCCTG ACGCTATGGT T

21

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.35 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

GCKCGGCGCT GCCACTCAGG

20

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.35t primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

GCTCGGCGCT GCCACTCAGG

20

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.36 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

ACGCCGAGAC CAAGCACTTC

20

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.38 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

CCAAAGAGGT GGCTTCTTCG

20

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.39 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

AAGGCCAGCA CGTTCTTCGC

20

(2) INFORMATION FOR SEQ ID NO:413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.40 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

CACGTTCGTG CGGCGCCCTG

19

(2) INFORMATION FOR SEQ ID NO:414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.41 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

CCTTCACCAC CAGCGTGCG

19

(2) INFORMATION FOR SEQ ID NO:415:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.42 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

GGCGACGACG TGCTGGTTC

19

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.43 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

GGCTCAGGGG CAGCGCCAC

19

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.44 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

CTGGCAGGTG TACGGCTTC

19

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.45 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

GCGTGGACCG AGTGACCGTG GTTTC

25

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.46 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

GACGTGGTGG CCGCGATGTG G

21

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "TCP1.47 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

~~GAAGTCTGCC~~
GTTCCCCAAG AG

22

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.48 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

CACACCACAC AGAAACCACG GTCAC

25

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.49 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

CGCCCCCTCC TTCCGCCAGG T

21

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.50 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

CGAAGCCGAA GGCCAGCACG TTCTT

25

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "TCP1.51 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

GGTGGCCCGA GTGCTGCAGA GG

22

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.52 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

GTAGCTGCGC ACGCTGGTGG TGAAG

25

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "TCP1.53 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

TGGGCGACGA CGTGCTGGTT CA

22

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.54 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

TATGGTTCCA GGCCCGTTCG CATCC

25

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "TCP1.55 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

CCAGCTGCGC CTACCAGGTG TGC

23

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.56 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

GCCCTCCCTG ACGCTATGGT TCCAG

25

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "TCP1.57 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GGTGCTGCCG CTGGCCACGT TCG

23

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.58 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

TCCCAGGGCA CGCACACCAG GCACT

25

(2) INFORMATION FOR SEQ ID NO:432:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.59 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

GTACAGGGCA CACCTTGTT CACTC

25

(2) INFORMATION FOR SEQ ID NO:433:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.60 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

TCGACGACGT ACACACTCAT CAGCC

25

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCPl.61 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

AGCGGCAGCA CCTCGCGGTA GTGGC

25

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCPl.62 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

CCACCAGCTC CTTCAGGCAG GACAC

25

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCPl.63 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

CCAGGGCTTC CCACGTGCGC AGCAG

25

(2) INFORMATION FOR SEQ ID NO:437:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.64 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

CGCACGAACG TGGCCAGCGG CAGCA

25

(2) INFORMATION FOR SEQ ID NO:438:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "TCP1.65 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

TGACCGTGGT TTCTGTGTGG TGT

23

(2) INFORMATION FOR SEQ ID NO:439:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.66 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

CCCTCTTCAA GTGCTGTCTG ATTCC

25

(2) INFORMATION FOR SEQ ID NO:440:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.67 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

ATCGCGGCCA CCACGTCCCT

20

(2) INFORMATION FOR SEQ ID NO:441:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.68 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

TGCTCCAGAC ACTCGGCCGG TAGAA

25

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.69 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

ACGAAGCCGT ACACCTGCC

19

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.72 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

CGACATCCCT GCGTTCTTGG CTTTC

25

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.73 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

CACTGCTGGC CTCATTAGG G

21

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "TCP1.74 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

CCGACATGGA GAACAAGC

18

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.75 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

GCAGCCATAAC TCAGGGACAC

20

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.76 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

CCATCCTCTC CACGCTGCTC

20

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.77 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

GGATGACCT CCGTGAGCCT G

21

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.78 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

CCAGGACAG GCTCACGGA

19

2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "billTCP1 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

CCTCTTCAAG TGCTGTCTGA TTCC

24

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "billTCP2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

CAGCTCGACG ACGTACACAC TCATC

25

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "billTCP4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

CTGACGTCCA GACTCCGCTT CAT

23

(2) INFORMATION FOR SEQ ID NO:453:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..33
- (D) OTHER INFORMATION: /note= "rpprim01 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

GACCTGAGCA GCTCGACGAC GTACACACTC ATC

33

(2) INFORMATION FOR SEQ ID NO:454:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Ltl primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

GTCGTCGAGC TGCTCAGGTC

20

(2) INFORMATION FOR SEQ ID NO:455:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Lt2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

AGCACGCTGA ACAGTGCCTT

20

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Lt3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GACCTGAGCA GCTCGACGAC

20

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Lt4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

AAGGCACTGT TCAGCGTGCT

20

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Lt5 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

CGGCCGAGTG TCTGGAGCAA

20

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "Lt6 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

GGATGAAGCG GAGTCTGGA

19

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "BamH1Lt7 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

ATGGATCCGT CGTCGAGCTG CTCAGGTCT

29

(2) INFORMATION FOR SEQ ID NO:461:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "SallLt8 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

ATCAGCTGAG CACGCTGAAC AGTGCCTTC

29

(2) INFORMATION FOR SEQ ID NO:462:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "K303 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

GTCTCCGTGA CATAAAAGAA AGAC

24

(2) INFORMATION FOR SEQ ID NO:463:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "K304 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

GCCAAGTTCC TGCACGGCT

20

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "K305 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

GCCTGTTCTT TTGAAACGTG GTCT

24

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "K306 primer"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = guanosine substituted by two biotin groups"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

NCCTGTTCTT TTGAAACGTG GTCT

24

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "K311 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

GTCAAGATGC CTGAGATAGA AC

22

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "K312 and K313 primers"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

TGCTTAGCTT GTGGGGGTGT CA

22

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "K320 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

GCTGCGTCCT GCTGCGCACG T

21

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "K321 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

CAGCGGGGAG CGCGCGGCAT C

21

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "K322 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

TGGGCCACCA GCGCGCGGAA A

21

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "slanti.1 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

CGGCCGCAGC CCGTCAGGCT TGGGG

25

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "slanti.2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

CCGACAGCTC CCGCAGCTGC ACCC

24

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "slanti.3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

CGTACACACT CATCAGCCAG TGCAGGAAC TGGC

34

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: /note= "slanti.4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

CGCGCCCGCT CGTAGTTGAG CACGCTGAAC AGTGCCTTCA CCCTCG

46

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "slanti.5 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

GCCCAGTCTG GACGTCAGCA GGGCGGGCCT GGCTTCCCG

39

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "UTR2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

ATTTGACCCA CAGGGACCCC CATCCAG

27

(2) INFORMATION FOR SEQ ID NO:477:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "FW5 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

ATGACCGCCC TCCTCGTGAG

20

(2) INFORMATION FOR SEQ ID NO:478:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "Nam1 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

GCCACCCCCCG CGATGCC

17

(2) INFORMATION FOR SEQ ID NO:479:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "Nam2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

AGCCCTGGCC CCGGCCA

17

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "Nam3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

TCCCACGTGC GCAGCAG

17

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "Nam4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

AGCAGGACGC AGCGCTG

17

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "PE01 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

CGCGGTAGTG GCTGCGCAGC AGGGAGCGCA CGGC

34

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "PE02 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

CCAGGGCTTC CCACGTGCGC AGCAGGACGC AGCGC

35

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: /note= "LM101 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

CTAGTCTAGA TCRCTAGCGT AATCTGGAAC ATCGTATGGG TRTCCAGGAT GGTCTTGAAG	60
TC	62

(2) INFORMATION FOR SEQ ID NO:485:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "LM103 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

TACCATGGGC TACCCATACG ACGTTCCAGA TTACCGCTCA	39
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(2) INFORMATION FOR SEQ ID NO:486:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "LM104 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

TATGAGCGTA ATCTGGAACG TCGTATGGGT AGCCCATGG	39
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(2) INFORMATION FOR SEQ ID NO:487:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: /note= "LM105 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

GTGTACGTCG TCGAGCTCCT CAGGTCTGCC TTTTATGTCA CGGAG

45

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: /note= "LM106 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

GTGTACGTCG TCGAGCTCCT CAGGTCTTTC GCTTATGTCA CGGAGACC

48

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: /note= "LM107 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

CCTCAGGTCT TTCTTGCTG TCACGGAGAC AACGTTCAA AAGAACAG

48

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "LM108 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

GGTCTTTCTT TTATGTCGCG GAGACAAACGT TTCAAAAGAA CAG

43

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: /note= "LM109 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

CTTTCTTTA TGTCACGGCG ACAACGTTTC AAAAGAACAG

40

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: /note= "LM_FFYTE primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

ATGAGTGTGT ACGTCGTCGA GCTCCTCAGG TCTACCACGT TTCAAAAGAA CAGGCTCTT	60
TTC	63

(2) INFORMATION FOR SEQ ID NO:493:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP061 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

GGCTGATGAG TGTGTACGTC GTCGA	25
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(2) INFORMATION FOR SEQ ID NO:494:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "HUM01 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

ACGTGGTCTC CGTGACATAA AAGAA	25
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(2) INFORMATION FOR SEQ ID NO:495:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "HUMO2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

AGGTCTTC TTTATGTCAC GGA

23

(2) INFORMATION FOR SEQ ID NO:496:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "HUMO3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

CACAGACCCC CGTCGCCTGG TC

22

(2) INFORMATION FOR SEQ ID NO:497:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "HUMO4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

CGGAGTCTGG ACGTCAGCAG GGC

23

(2) INFORMATION FOR SEQ ID NO:498:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "SLW F1N primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

CGCGGATCCG TAACTAAAAT GCCGCGCGCT CCCCCGCTGC

39

(2) INFORMATION FOR SEQ ID NO:499:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: /note= "SLW F1C primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

CCGGAATTCTG TTAGTTACTT ACAAAAGAGGT GGCTTCTTCG GC

42

(2) INFORMATION FOR SEQ ID NO:500:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "SLW F2N primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

CGCGGATCCG TAACTAAAGC CACCTCTTG GAGGGTGCG

39

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: /note= "SLW F2C primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

CCGGAATTCTG TTAGTTACTT AAGACCTGAG CAGCTCGACG AC

42

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "SLW F3N primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

CGCGGATCCG TAACTAAAAT GAGTGTGTAC GTCTCGAG

39

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: /note= "SLW F3C primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

CCGGAATTCTG TTAGTTACTT AGATCCCCTG GCACCTGGACG

40

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "SLW F4N primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

CGCGGATCCG TAACTAAAAT CCCGCAGGGC TCCATCCTC

39

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: /note= "SLW F4C primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

CCGGAATTCTG TTAGTTACTT AGTCCAGGAT GGTCTTGAAG TC

42

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "40-60 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

GGCATCGCGG GGGTGGCCGG G

21

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "260-280 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GCACACCTGG CGGAAGGGAGG G

21

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "500-520 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

GCGTGCCAGC AGGTGAAACCA G

21

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "770-790 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

CTCAGGGGCA GCGCCACGCC T

21

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "885-905 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

AGGTGGCTTC TTCGGCGGGT C

21

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "1000-1020 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

GGACAAGGCG TGCCCCAGGG A

21

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "1300-1320 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

GCTGGGGTGA CCGCAGCTCG C

21

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "1520-1540 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

GATGAACCTTC TTGGTGTCC T

21

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "2110-2130 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

GTGCGCCAGG CCCTGTGGAT A

21

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "2295-2315 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GCCCATGGGC GGCCTTCTGG A

21

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "2450-2470 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

GAGGCCACTG CTGGCCTCAT T

21

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "2670-2690 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

CGGTGAGGTG AGGTGTCACC A

21

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /note= "3080-3110 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

GCTGCAGCAC ACATGCGTGA AACCTGTACG C

31

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "3140-3160 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

GACGGCGCAGG AAAATGTGG G

21

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "3690-3710 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

CCGAGGCCA GCCTGTGGGG A

21

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "55-75 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

CAGCGGGGAG CGCGCGGCAT C

21

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "151-171 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

CAGCACCTCG CGGTAGTGGC T

21

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "TP1.1 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

TCAAGCCAAA CCTGAATCTG AG

22

(2) INFORMATION FOR SEQ ID NO:524:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TP1.2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

CCCGAGTGAA TCTTTCTACG C

21

(2) INFORMATION FOR SEQ ID NO:525:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "TP1.3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

GTCTCTGGCA GTTCCCTCAT CCC

23

(2) INFORMATION FOR SEQ ID NO:526:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "TP1.4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

TTAGGCATC CTCCCAAGCA CA

22

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

TTAGGGTTAG

10

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

TTAGGGTTAG GGTTAGGG

18

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

GTTAGGGTTA GGGTTAGG

18

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: repeat_unit
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "sequence (CCCTAA)-n, where n is at least 1, or at least 3, or at least 10 or more"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

CCCTAACCT AACCTAACCC CTAACCCCTAA CCCTAACCT AACCTAACCC CTAACCCCTAA 60

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (X)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN TTAG 34

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (X)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN AGGG 34

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (X)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN TTAGGGTTAG 40

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (X)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN TTAGGGTTAG GGTTAG 46

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (X)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN TTAGGGTTAG GGTTAGGGTT AG

52

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (X)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN TTAGGGTTAG GGTTAGGGTT AGGGTTAG

58

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..10
- (D) OTHER INFORMATION: /note= "primer terminating at template boundary"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

TAGGGATTAG

10

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "primer for hTRT nucleolytic assay"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = 3'-deoxyguanosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

TTAGGGTTAG GGTTAN

16

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: repeat_unit
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "sequence (TTAGGG)-n, where n is 1-10, or typically 3-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

TTAGGGTTAG GGTTAGGGTT AGGGTTAGGG TTAGGGTTAG GGTTAGGGTT AGGGTTAGGG

60

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

Trp	Xaa	Gly	Xaa	Ser
1				5

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

Pro	Arg	Arg	Arg
i			

q2

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

Pro	Lys	Arg	Pro	Arg	Arg
1					5

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "antisense hTRT molecule"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

GCTCTAGAACAT GAAGGGTG

18

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "S1 control oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

GCGACGACTG ACATTGGCCG G

21

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "S2 control oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

GGCTCGAAGT AGCACCGGTG C

21

(2) INFORMATION FOR SEQ ID NO:546:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "S3 control oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

GTGGGAACAG GCCGATGTCC C

21

(2) INFORMATION FOR SEQ ID NO:547:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "ON1 oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

TCCCACGTGC GCAGCAGGAC GCAGCGCTGC

30

(2) INFORMATION FOR SEQ ID NO:548:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "ON2 oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

GCCGGGGCCA GGGCTTCCCA CGTGCGCAGC

30

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "ON3 oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

GGCATCGCGG GGGTGGCCGG GGCCAGGGCT

30

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "delta-182 species specific primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

GGCACTGGAC GTAGGACGTG

20

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "293 cell line lambda cDNA library PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

CGGAAGACTG TCTGGAGCAA

20

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "GAPDH control primer K136"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

CTCAGACACC ATGGGAAAGG TGA

23

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "GAPDH control primer K137"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

ATGATCTTGA GGCTGGTC ATA

23

(2) INFORMATION FOR SEQ ID NO:554:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /note= "competitor oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

TAGACCTGTT AGTGACATT TGAATTGAAG C

31

(2) INFORMATION FOR SEQ ID NO:555:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "competitor oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

TAGACCTGTT AGGTTGGATT TGTGGCATCA

30

(2) INFORMATION FOR SEQ ID NO:556:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "biotin-labeled telomerase-specific oligonucleotide"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = thymidine modified by a biotin group"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 12..13
- (D) OTHER INFORMATION: /mod_base= gm

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 14..17
- (D) OTHER INFORMATION: /mod_base= um

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 18..21
- (D) OTHER INFORMATION: /mod_base= gm

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 22..25
- (D) OTHER INFORMATION: /mod_base= um

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 26
- (D) OTHER INFORMATION: /mod_base= gm

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

NAGACCTGTT ANNNNNNNNN NNNNNN

26

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /note= "displacement deoxyoligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

CAAAACCCA AAACCTAACCA GGTCTA

26

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: /note= "5' primer encoding a hammerhead ribozyme, a T7-promoter and an EcoR1 site"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

GCGGGAATTCTAATACGACTCACTATAGGG AAGAAACTCT GATGAGGCCG AAAGGCCGAA 60

ACTCCACGAA AGTGGAGTAA GTTTCTCGAT AATTGATCTG TAG 103

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "3' primer including an EarI site and a BamH1 site"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

CGGGGATCCT CTTCAAAAGA TGAGAGGACA GCAAAC 36

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

CCCCAAAACC CCAAAACCCC AAAACCCCA CAGGGTTTT GGGGTTTTGG GGTTTGGGG 60

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

CCAAAACCCC AAAACCCCAA AACCCCCACA GGGGTTTTGG GGTTTGGGG TTTTGGGG 58

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

AAAAACCCCAA AACCCCAAAA CCCCCACAGG GTTTGGGG TTTTGGGGTT TTGGGG 56

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

AACCCCAAAA CCCCAAAACC CCCACAGGGG TTTTGGGGTT TTGGGGTTTT GGGG

54

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

CCCCAAAACC CCAAAACCCC CACAGGGGTT TTGGGGTTTT GGGGTTTT

48

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

AAAACCCCAA AACCCCAAAA CCCCCACAGG GGTTTGGGG TTTTGGGTT TT

52

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

AACCCCAAAA CCCCAAAACC CCCACAGGGG TTTTGGGTT TTGGGGTTT

50

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

CCAAAACCCC AAAACCCCCA CAGGGTTTT GGGGTTTGG GGTTTT

46

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..44
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

AAACCCCAA AACCCCCACA GGGGTTTGGG GGTTTGGGG TTTT

44

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "degenerate oligonucleotide primer for cloning of Euplotes telomerase 123 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

TCTRAARTAR TGDTGNADRT TRTTCAT

27

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /note= "degenerate oligonucleotide primer for cloning of Euplotes telomerase 123 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

GCGGATCCAT GAAYCCWGAR AAYCCWAAYG T

31

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "degenerate oligonucleotide primer for cloning of Euplotes telomerase 43 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

NNNGTNACHG GHATHAAYAA

20

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "degenerate oligonucleotide primer for cloning of Euplotes telomerase 43 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

DGCDGTYTCY TGRTCRTTRT A

21

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "degenerate oligonucleotide primer for cloning of Oxytricha trifallax telomerase homologous to Euplotes 123 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:574:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "degenerate oligonucleotide primer for cloning of Oxytricha trifallax telomerase homologous to Euplotes 123 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

DGTDATNARN ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:575:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "K231 forward primer"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = guanosine modified by a biotin group"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

NCCTATTTYT TYTAYNNNAC NGA

23

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "K220 reverse primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

CCAGATATNA DNARRAARTC RTC

23

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe, Ile or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

Asp	Asp	Phe	Leu	Xaa	Ile
1		5			

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "K228 forward primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

ACAAATGMGNH TNHTNCCNAA RAA

23

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2..3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

Arg Xaa Xaa Pro Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "K224 reverse primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

ACGAATCKNG GDATNSWRTE RTARCA

26

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

Cys	Tyr	Asp	Ser	Ile	Pro	Arg
1				5		

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "K227 reverse primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

CAATTCTCRT ARCANSWYTT DATRTC

26

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

Asp	Ile	Lys	Ser	Cys	Tyr	Asp
1				5		

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..269
- (D) OTHER INFORMATION: /note= "clone 168-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

GATTACTCCC GAAGAAAGGA TCTTCCGTC CAATCATGAC TTTCTTAAGA AAGGACAAGC	60
AAAAAAATAT TAAGTAAAT CTAAATTAAA TTCTAATGGA TAGCCAACCT GTGTTTAGGA	120
ATTTAAAAGA CATGCTGGGA TAAAAGATAG GATACTCAGT CTTTGATAAT AAACAAATTT	180
CAGAAAAATT TGCCTAATTC ATAGAGAAAT GGAAAAATAA AGGAAGACCT CAGCTATATT	240
ATGTCACTCT AGACATAAAG ACTTGCTAC	269

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "K297 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

GAGTGACATA ATATACGTGA	20
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(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..474
- (D) OTHER INFORMATION: /note= "Tetrahymena DNA fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

AAACACAAGG AAGGAAGTCA AATATTCTAT TACCGTAAAC CAATATGGAA ATTAGTGAGT	60
AAATTAAC TA TTGTCAAAGT AAGAATTAG TTTCTGAAA AGAATAAATA AATGAAAAAT	120
AATTTTATC AAAAATTTA GCTTGAAGAG GAGAATTGG AAAAAGTTGA AGAAAAATTG	180
ATACCAGAAG ATTCATTTA GAAATACCC CAAGGAAAGC TAAGGATTAT ACCTAAAAAA	240
GGATCTTCC GTCCAATCAT GACTTCTTA AGAAAGGACA AGCAAAAAAA TATTAAGTTA	300
AATCTAAATT AAATTCTAAT GGATAGCCAA CTTGTGTTA GGAATTAAA AGACATGCTG	360
GGATAAAAGA TAGGATACTC AGTCTTGAT AATAAACAAA TTTCAGAAAA ATTTGCCTAA	420
TTCATAGAGA AATGGAAAAA TAAAGGAAGA CCTCAGCTAT ATTATGTCAC TCTA	474

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: /note= "Q-T primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

CCAGTGAGCA GAGTGACGAG GACTCGAGCT CAAGCTTTT TTTTTTTT	50
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(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "Q-O primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

CCAGTGAGCA GAGTGACG

18

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "M2-T primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

GTGTCATTTC TATATGGAAG ATTTGATTGA TG

32

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "Q-I primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

GAGGACTCGA GCTCAAGC

18

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "M2-T2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

ACCTATCGTT TACGAAAAAG AAAGGATCAG TG

32

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "M2-B primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

CACTGATCCT TTCTTTTCG TAAACGATAG GT

32

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /note= "M2-B2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

CATCAATCAA ATCTTCCATA TAGAAATGAC A

31

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "PCR Adapt SfiI primer"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = 5'-phosphorylated guanosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

NGGCCGTGTT GGCCTAGTTC TCTGCTC

27

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: /note= "PCR Adapt SfiII primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

GAGGAGGAGA AGAGCAGAGA ACTAGGCCAA CACGCC

38

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

ATGCTCCTGC GTTTGGTGG

19

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "F3b primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

TCTAACCCATA ACTGAGAAGG GCGTAG

26

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "R3c primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

GTTTGCTCTA GAATGAACGG TGGAAG

26

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: /note= "104-base intronic sequence (SEQ ID NO:7) inserted at the junction corresponding to bases 274 and 275 of hTRT (SEQ ID NO:1)"

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 28..131
- (D) OTHER INFORMATION: /note= "intronic sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

CCCCCCGCCG CCCCCTCCTT CCGCCAGGTG GGCCTCCCCG GGGTCGGCGT CCGGCTGGGG 60

TTGAGGGCGG CGGGGGGAA CCAGCGACAT GCGGAGAGCA GCGCAGGCCA CTCAGGGCGC 120

TTCCCCCGCA GGTGT CCTGC CTGAAGGAGC TGGTGGCCCG AGTGCTGCAG 170

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..1285
- (D) OTHER INFORMATION: /note= "fusion protein composed of enterokinase cleavable, His tagged thioredoxin moiety and full length hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp
 1 5 10 15

Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala His Trp
 20 25 30

Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
 35 40 45

Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Arg Ile Asp His Asn
 50 55 60

Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu
 65 70 75 80

Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
 85 90 95

Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly
 100 105 110

Ser Gly Asp Asp Asp Asp Lys Val Pro Met His Glu Leu Glu Ile Phe
 115 120 125

Glu Phe Ala Ala Ala Ser Thr Gln Arg Cys Val Leu Leu Arg Thr Trp
 130 135 140

Glu Ala Leu Ala Pro Ala Thr Pro Ala Met Pro Arg Ala Pro Arg Cys
 145 150 155 160

Arg Ala Val Arg Ser Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro
 165 170 175

Leu Ala Thr Phe Val Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val
 180 185 190

Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu
 195 200 205

Val Cys Val Pro Trp Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe
 210 215 220

Arg Gln Val Ser Cys Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg
 225 230 235 240

Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe Gly Phe Ala Leu
 245 250 255

Leu Asp Gly Ala Arg Gly Pro Pro Glu Ala Phe Thr Thr Ser Val
 260 265 270

Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly
 275 280 285

Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His
 290 295 300

Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala
 305 310 315 320

Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp
 500 505 510
 Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln
 515 520 525
 Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly
 530 535 540
 Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys
 545 550 555 560
 Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu
 565 570 575
 Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro
 580 585 590
 Gly Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile
 595 600 605
 Leu Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu
 610 615 620
 Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg
 625 630 635 640
 Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
 645 650 655
 Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala
 660 665 670
 Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg
 675 680 685
 Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met
 690 695 700
 Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu
 705 710 715 720
 Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu
 725 730 735
 Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp
 740 745 750
 Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln
 755 760 765
 Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala
 770 775 780
 Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
 785 790 795 800
 Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln
 805 810 815

Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
 820 825 830
 Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
 835 840 845
 Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
 850 855 860
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 865 870 875 880
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 885 890 895
 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
 900 905 910
 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
 915 920 925
 Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
 930 935 940
 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
 945 950 955 960
 Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
 965 970 975
 Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
 980 985 990
 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
 995 1000 1005
 Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala
 1010 1015 1020
 Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg
 1025 1030 1035 1040
 Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp
 1045 1050 1055
 Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
 1060 1065 1070
 Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro
 1075 1080 1085
 Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
 1090 1095 1100
 Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala
 1105 1110 1115 1120
 Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu
 1125 1130 1135

Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln
 325 330 335
 Ala Arg Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys
 340 345 350
 Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly
 355 360 365
 Leu Pro Ala Pro Gly Ala Arg Arg Gly Gly Ser Ala Ser Arg Ser
 370 375 380
 Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu
 385 390 395 400
 Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg
 405 410 415
 Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala
 420 425 430
 Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser
 435 440 445
 His Pro Ser Val Gly Arg Gln His His Ala Gly Pro Pro Ser Thr Ser
 450 455 460
 Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu
 465 470 475 480
 Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro
 485 490 495
 Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg
 500 505 510
 Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr
 515 520 525
 Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro
 530 535 540
 Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val
 545 550 555 560
 Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala
 565 570 575
 Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu
 580 585 590
 Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His
 595 600 605
 Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg
 610 615 620
 Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe
 625 630 635 640

Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu
 645 650 655
 Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp
 660 665 670
 Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg
 675 680 685
 Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val
 690 695 700
 Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
 705 710 715 720
 Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys
 725 730 735
 Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg
 740 745 750
 Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala
 755 760 765
 Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg
 770 775 780
 Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg
 785 790 795 800
 Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser
 805 810 815
 Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser
 820 825 830
 Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu
 835 840 845
 Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val
 850 855 860
 Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu
 865 870 875 880
 Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg
 885 890 895
 Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe
 900 905 910
 Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln
 915 920 925
 Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val
 930 935 940
 Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp
 945 950 955 960

Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
 965 970 975
 Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr
 980 985 990
 Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala
 995 1000 1005
 Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu
 1010 1015 1020
 Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu
 1025 1030 1035 1040
 Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr
 1045 1050 1055
 Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe
 1060 1065 1070
 Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu
 1075 1080 1085
 Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg
 1090 1095 1100
 Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly
 1105 1110 1115 1120
 Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His
 1125 1130 1135
 Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr
 1140 1145 1150
 Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys
 1155 1160 1165
 Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe
 1170 1175 1180
 Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu
 1185 1190 1195 1200
 Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly
 1205 1210 1215
 Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu
 1220 1225 1230
 Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser
 1235 1240 1245
 Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr
 1250 1255 1260
 Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe
 1265 1270 1275 1280

Lys Thr Ile Leu Asp
1285

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

Gly Ser Val Thr Lys
1 5

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..538
- (D) OTHER INFORMATION: /note= "fusion protein composed of glutathione-S-transferase sequence, thrombin cleavage sequence, recognition sequence for heart muscle protein kinase, residues introduced by cloning and hTRT protein fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15

Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80

Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
							85				90				95
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
							100				105				110
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
							115				120				125
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
							130				135				140
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
							145				150				160
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
							165				170				175
Val	Cys	Phe	Lys	Lys	Arg	Ile	Gl <u>u</u>	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
							180				185				190
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
							195				200				205
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
							210				215				220
Gly	Ser	Arg	Arg	Ala	Ser	Val	Gly	Ser	Val	Thr	Lys	Ile	Pro	Gln	Gly
							225				230				240
Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp	Met	Gl
							245				250				255
Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu	Arg	Leu	
							260				265				270
Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala	Lys	Thr
							275				280				285
Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	Val
							290				295				300
Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu	Asp	Glu	Ala	Leu
							305				310				320
Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly	Leu	Phe	Pro	Trp
							325				330				335
Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val	Gln	Ser	Asp	Tyr
							340				345				350
Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	Arg	Ala	Ser	Val	Thr	Phe	Asn	Arg
							355				360				365
Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	Arg	Arg	Lys	Leu	Phe	Gly	Val	Leu
							370				375				380
Arg	Leu	Lys	Cys	His	Ser	Leu	Phe	Leu	Asp	Leu	Gln	Val	Asn	Ser	Leu
							385				390				400

Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr
 405 410 415

 Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp
 420 425 430

 Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu
 435 440 445

 Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala
 450 455 460

 Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys
 465 470 475 480

 His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val
 485 490 495

 Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys
 500 505 510

 Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala
 515 520 525

 Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 530 535

(2) INFORMATION FOR SEQ ID NO:603:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 530 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..530
 - (D) OTHER INFORMATION: /note= "fusion protein composed of glutathione-S-transferase sequence, thrombin cleavage sequence, recognition sequence for heart muscle protein kinase, residues introduced by cloning, eight consecutive His residues and hTRT protein fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30

 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205

Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220

Gly Ser Arg Arg Ala Ser Val Gly Ser Val His His His His His His
 225 230 235 240

His His Gly Ser Val Thr Lys Met Ser Val Tyr Val Val Glu Leu Leu
 245 250 255

Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu
 260 265 270

Phe Phe Tyr Arg Pro Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile
 275 280 285

Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu
 290 295 300

Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu
 305 310 315 320

Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp
 325 330 335

Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg
 340 345 350

Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg
 355 360 365

Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp
 370 375 380
 Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp
 385 390 395 400
 Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr
 405 410 415
 Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile
 420 425 430
 Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys
 435 440 445
 Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr
 450 455 460
 Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln
 465 470 475 480
 Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser
 485 490 495
 Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met
 500 505 510
 Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln
 515 520 525
 Gly Ile
 530

(2) INFORMATION FOR SEQ ID NO:604:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 515 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..515
 - (D) OTHER INFORMATION: /note= "fusion protein composed of glutathione-S-transferase sequence, thrombin cleavage sequence, recognition sequence for heart muscle protein kinase, residues introduced by cloning and hTRT protein fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205

Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220

Gly Ser Arg Arg Ala Ser Val Gly Ser Val Thr Lys Met Ser Val Tyr
 225 230 235 240

Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe
 245 250 255

Gln Lys Asn Arg Leu Phe Phe Tyr Arg Pro Ser Val Trp Ser Lys Leu
 260 265 270

Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu
 275 280 285

Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu
 290 295 300

Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro
 305 310 315 320

Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu
 325 330 335

Lys Arg Ala Glu Arg Leu Thr Ser Arg Lys Ala Leu Phe Ser Val Leu
 340 345 350

Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu
 355 360 365

Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val
 370 375 380

Arg Ala Gln Asp Pro Pro Glu Tyr Phe Val Lys Val Asp Val Thr
 385 390 395 400

Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala
 405 410 415

Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 420 425 430

Val Gln Lys Ala Ala His Gly Val Arg Lys Ala Phe Lys Ser His Val
 435 440 445

Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His
 450 455 460

Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser
 465 470 475 480

Ser Ser Leu Asn Glu Ala Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 485 490 495

Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 500 505 510

Gln Gly Ile
 515

(2) INFORMATION FOR SEQ ID NO:605:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 514 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..515
 - (D) OTHER INFORMATION: /note= "fusion protein composed of glutathione-S-transferase sequence, thrombin cleavage sequence, recognition sequence for heart muscle protein kinase, residues introduced by cloning and hTRT protein fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205

Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220

Gly Ser Arg Arg Ala Ser Val Gly Ser Val Thr Lys Ala Thr Ser Leu
 225 230 235 240

Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg
 245 250 255

Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp
 260 265 270

Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr
 275 280 285

Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser
 290 295 300

Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe
 305 310 315 320

Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg
 325 330 335

Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu
 340 345 350

Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys
 355 360 365

Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu
 370 375 380

Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro
 385 390 395 400

Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val
 405 410 415

Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu
 420 425 430

Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys
 435 440 445

Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr
 450 455 460

Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly
 465 470 475 480

Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu
 485 490 495

Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
 500 505 510

Arg Ser

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..517
- (D) OTHER INFORMATION: /note= "fusion protein composed of glutathione-S-transferase sequence, thrombin cleavage sequence, recognition sequence for heart muscle protein kinase, residues introduced by cloning and hTRT protein fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205

Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220

Gly Ser Arg Arg Ala Ser Val Gly Ser Val Thr Lys Met Pro Arg Ala
 225 230 235 240

Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Ser His Tyr Arg Glu Val
 245 250 255

Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro Gln Gly Trp Arg
 260 265 270

Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln
 275 280 285

Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro Ala Ala Pro Ser
 290 295 300

Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val Ala Arg Val Leu Gln
 305 310 315 320

Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe Gly Phe Ala
 325 330 335
 Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Thr Thr Ser Val
 340 345 350
 Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly
 355 360 365
 Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His
 370 375 380
 Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala Pro Cys Ala Tyr
 385 390 395 400
 Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala
 405 410 415
 Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu
 420 425 430
 Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu
 435 440 445
 Pro Ala Pro Gly Ala Arg Arg Gly Ser Ala Ser Arg Ser Leu
 450 455 460
 Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg
 465 470 475 480
 Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly
 485 490 495
 Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu
 500 505 510
 Glu Ala Thr Ser Leu
 515

(2) INFORMATION FOR SEQ ID NO:607:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..30
 - (D) OTHER INFORMATION: /note= "oligonucleotide used to modify hTRT cDNA nucleotides 779 to 781 from GCG to CAT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

CCGGGCCACCC CCCATATGCC GCGCGCTCCC

30

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: /note= "oligonucleotide used to create expression vectors pGRN127, pGRN128 and pGRN130"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

TGCGCACGTG GGAAGCCCTG GCAGATCTGA ATTCCACCAT GCCGCGCGCT CCCCCGCTG

58

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: /note= "oligonucleotide used to create expression vectors pGRN129 and pGRN130"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

CGGGACGGGC TGCTCCTGCG TTTGGTGGAC GCGTTCTTGT TGGTGACACC TCACCTCACC

60

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

Asn Ser Ala Val Asp
1 5

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..1154
- (D) OTHER INFORMATION: /note= "fusion protein composed of hTRT protein sequence, vector sequences, the Myc epitope and His6 tag"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560

Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700

Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720

Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735

Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750

Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765

Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780

Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910
 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925
 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940
 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
 945 950 955 960
 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975
 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Gln
 995 1000 1005
 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
 1010 1015 1020
 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
 1025 1030 1035 1040
 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
 1045 1050 1055
 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
 1060 1065 1070
 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
 1075 1080 1085
 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
 1090 1095 1100
 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Asn
 1105 1110 1115 1120
 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp Leu Glu Gln Lys
 1125 1130 1135

Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His
 1140 1145 1150
 His His

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..1200
- (D) OTHER INFORMATION: /note= "fusion protein composed of His6 and Anti-Xpress tags, enterokinase cleavage site and full length hTRT protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

Met Pro Arg Gly Ser His His His His His His Gly Met Ala Ser Met
 1 5 10 15

Thr Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Leu
 20 25 30

Asp Pro Ser Ser Arg Ser Ala Ala Gly Thr Met Glu Phe Ala Ala Ala
 35 40 45

Ser Thr Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu Ala Pro
 50 55 60

Ala Thr Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser
 65 70 75 80

Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val
 85 90 95

Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro
 100 105 110

Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp
 115 120 125

Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys
 130 135 140

Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly
 145 150 155 160

Ala Lys Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg
 165 170 175

Gly Gly Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro
 180 185 190
 Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu
 195 200 205
 Leu Arg Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys
 210 215 220
 Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly
 225 230 235 240
 Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro
 245 250 255
 His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn
 260 265 270
 His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly
 275 280 285
 Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys
 290 295 300
 Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly
 305 310 315 320
 Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg
 325 330 335
 Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser
 340 345 350
 Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly
 355 360 365
 Arg Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro
 370 375 380
 Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu
 385 390 395 400
 Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser
 405 410 415
 Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile
 420 425 430
 Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro
 435 440 445
 Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu
 450 455 460
 Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His
 465 470 475 480
 Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg
 485 490 495

Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg
 1140 1145 1150
 His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln
 1155 1160 1165
 Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu
 1170 1175 1180
 Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1185 1190 1195 1200

(2) INFORMATION FOR SEQ ID NO:613:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1189 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..1189
- (D) OTHER INFORMATION: /note= "fusion protein composed of melittin signal sequence and full length hTRT protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
 1 5 10 15

Ser Tyr Ile Tyr Ala Asp Pro Ser Ser Arg Ser Ala Ala Gly Thr Met
 20 25 30

Glu Phe Ala Ala Ala Ser Thr Gln Arg Cys Val Leu Leu Arg Thr Trp
 35 40 45

Glu Ala Leu Ala Pro Ala Thr Pro Ala Met Pro Arg Ala Pro Arg Cys
 50 55 60

Arg Ala Val Arg Ser Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro
 65 70 75 80

Leu Ala Thr Phe Val Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val
 85 90 95

Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu
 100 105 110

Val Cys Val Pro Trp Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe
 115 120 125

Arg Gln Val Ser Cys Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg
 130 135 140

Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe Gly Phe Ala Leu
 145 150 155 160

Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe Thr Thr Ser Val
 165 170 175

Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly
 180 185 190

Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His
 195 200 205

Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala
 210 215 220

Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln
 225 230 235 240

Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys
 245 250 255

Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly
 260 265 270

Leu Pro Ala Pro Gly Ala Arg Arg Gly Gly Ser Ala Ser Arg Ser
 275 280 285

Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu
 290 295 300

Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg
 305 310 315 320

Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala
 325 330 335

Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser
 340 345 350

His Pro Ser Val Gly Arg Gln His His Ala Gly Pro Pro Ser Thr Ser
 355 360 365

Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu
 370 375 380

Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro
 385 390 395 400

Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg
 405 410 415

Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr
 420 425 430

Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro
 435 440 445

Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val
 450 455 460

Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala
 465 470 475 480
 Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu
 485 490 495
 Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His
 500 505 510
 Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg
 515 520 525
 Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe
 530 535 540
 Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu
 545 550 555 560
 Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp
 565 570 575
 Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg
 580 585 590
 Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val
 595 600 605
 Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
 610 615 620
 Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys
 625 630 635 640
 Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg
 645 650 655
 Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala
 660 665 670
 Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg
 675 680 685
 Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg
 690 695 700
 Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser
 705 710 715 720
 Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser
 725 730 735
 Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu
 740 745 750
 Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val
 755 760 765
 Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu
 770 775 780

Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg
 785 790 795 800
 Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe
 805 810 815
 Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln
 820 825 830
 Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val
 835 840 845
 Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp
 850 855 860
 Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
 865 870 875 880
 Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr
 885 890 895
 Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala
 900 905 910
 Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu
 915 920 925
 Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu
 930 935 940
 Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr
 945 950 955 960
 Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe
 965 970 975
 Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu
 980 985 990
 Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg
 995 1000 1005
 Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly
 1010 1015 1020
 Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His
 1025 1030 1035 1040
 Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr
 1045 1050 1055
 Asn Ile Tyr Lys Ile Leu Leu Gln Ala Tyr Arg Phe His Ala Cys
 1060 1065 1070
 Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe
 1075 1080 1085
 Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu
 1090 1095 1100

Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly
 1105 1110 1115 1120
 Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu
 1125 1130 1135
 Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser
 1140 1145 1150
 Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr
 1155 1160 1165
 Leu Thr Ala Leu Glu Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe
 1170 1175 1180
 Lys Thr Ile Leu Asp
 1185

(2) INFORMATION FOR SEQ ID NO:614:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: /note= "oligonucleotide used to create expression vectors pGRN128 and pGRN129"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

CTGCCCTCAG ACTTCAAGAC CATCCTGGAC TACAAGGACG ACGATGACAA ATGAATTAG	60
ATCTGCGGCC GCCACCGCGG TGGAGCTCCA GC	92

(2) INFORMATION FOR SEQ ID NO:615:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: /note= "mutagenic oligo used to add a CSP45I site at the C-terminus of hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

CTTCAAGACC ATCCTGGACT TTCGAAACGC GGCCGCCACC GCGGTGGAGC TCC

53

(2) INFORMATION FOR SEQ ID NO:616:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..33
- (D) OTHER INFORMATION: /note= "oligonucleotide RA45"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

GCCACCCCCG CGCTGCCCTCG AGCTCCCCGC TGC

33

(2) INFORMATION FOR SEQ ID NO:617:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: /note= "primer hTR+1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

GGGGAAGCTT TAATACGACT CACTATAGGG TTGCGGAGGG TGGGCCTG

48

(2) INFORMATION FOR SEQ ID NO:618:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "primer hTR+445"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

CCCCGGATCC TGCGCATGTG TGAGCCGAGT CCTGGG

36

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: /note= "synthetic telomerase product"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

ATTCCGTCGA GCAGAGTTAG GGTTAGGGTT AGGGTTAGGG TTAGGGTTAG GGTTAGGGTT

60

AG

62

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "primer M2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

AATCCGTCGA GCAGAGTT

18

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "primer H3.03"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

TTAGGGTTAG GGTTAGGG

18

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

AATCCGTCGA GCACAGGG

18

(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

AATCCGTCGA GCAGATAG

18

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: /note= "T701 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

GGGAGATCTT AATACGACTC ACTATAGATT CAGGCCATGG TGCTGCGCCG GCTGTCAGGC	60
TCCCCACGACG TAGTCCATGT TCAC	84

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "reverse01 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

GGGTCTAGAT CGGGAAGAGT GTCTGGAGCA AG	32
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(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: /note= "T702 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

GGGAGATCTT AATACGACTC ACTATAGATT CAGGCCATGG TGCTGCGCCG GCTGTCAGGG	60
CGGCCTTCTG GACCACGGCA TACC	84

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "reverse02 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

GGTCTAGACG ATATCCACAG GGCCTGGCGC

30

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1407 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..1407
- (D) OTHER INFORMATION: /note= "fusion protein composed of enhanced green fluorescent protein (EGFP) residues, residues encoded by the 5' untranslated region of hTRT mRNA and hTRT protein sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1					5				10						15

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
					20				25				30		

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
					35			40				45			

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
					50			55			60				

Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
					65			70			75		80		

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240

 Gly Arg Thr Gln Ile Ser Ser Ser Phe Glu Phe Ala Ala Ser
 245 250 255

 Thr Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu Ala Pro Ala
 260 265 270

 Thr Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu
 275 280 285

 Leu Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg
 290 295 300

 Arg Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala
 305 310 315 320

 Ala Phe Arg Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp
 325 330 335

 Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu
 340 345 350

 Lys Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala
 355 360 365

 Lys Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly
 370 375 380

 Gly Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn
 385 390 395 400

Thr Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu
 405 410 415
 Arg Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala
 420 425 430
 Leu Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro
 435 440 445
 Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His
 450 455 460
 Ala Ser Gly Pro Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His
 465 470 475 480
 Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala
 485 490 495
 Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg
 500 505 510
 Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln
 515 520 525
 Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly
 530 535 540
 Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu
 545 550 555 560
 Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg
 565 570 575
 Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp
 580 585 590
 Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr
 595 600 605
 Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser
 610 615 620
 Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe
 625 630 635 640
 Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg
 645 650 655
 Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu
 660 665 670
 Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys
 675 680 685
 Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu
 690 695 700
 Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro
 705 710 715 720

Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val
 725 730 735
 Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu
 740 745 750
 Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys
 755 760 765
 Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr
 770 775 780
 Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly
 785 790 795 800
 Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu
 805 810 815
 Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
 820 825 830
 Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu
 835 840 845
 Phe Phe Tyr Arg Pro Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile
 850 855 860
 Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu
 865 870 875 880
 Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu
 885 890 895
 Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp
 900 905 910
 Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg
 915 920 925
 Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg
 930 935 940
 Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp
 945 950 955 960
 Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp
 965 970 975
 Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr
 980 985 990
 Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile
 995 1000 1005
 Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys
 1010 1015 1020
 Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr
 1025 1030 1035 1040

Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln
 1045 1050 1055
 Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser
 1060 1065 1070
 Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met
 1075 1080 1085
 Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln
 1090 1095 1100
 Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys
 1105 1110 1115 1120
 Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly.
 1125 1130 1135
 Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu
 1140 1145 1150
 Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu
 1155 1160 1165
 Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val
 1170 1175 1180
 Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His
 1185 1190 1195 1200
 Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu
 1205 1210 1215
 Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser
 1220 1225 1230
 Val Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys
 1235 1240 1245
 Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu
 1250 1255 1260
 Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu
 1265 1270 1275 1280
 Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe
 1285 1290 1295
 His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser
 1300 1305 1310
 Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly
 1315 1320 1325
 Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala
 1330 1335 1340
 Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His
 1345 1350 1355 1360

Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr
 1365 1370 1375

Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala
 1380 1385 1390

Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1395 1400 1405

(2) INFORMATION FOR SEQ ID NO:629:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "TS primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

AATCCGTCGA GCAGAGTT

18

(2) INFORMATION FOR SEQ ID NO:630:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "ACX primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

GCGCGGGCTTA CCCTTACCCCT TACCTAAACC

30

(2) INFORMATION FOR SEQ ID NO:631:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "U2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

ATCGCTTCTC GGCCTTT

18

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "TSU2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

AATCCGTCGA GCAGAGTTAA AAGGCCGAGA AGCGAT

36

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 Ala, Leu, Ile, Val, Pro, Phe,
 Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

Xaa Arg Xaa Xaa Pro Lys
1 5

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

Xaa Arg Xaa Ile Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 6
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 8
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

Pro Xaa Leu Tyr Phe Xaa Xaa Xaa Asp Xaa Xaa Xaa Cys Tyr Asp Xaa
1 5 10 15

Ile

(2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 Ala, Leu, Ile, Val, Pro, Phe,
 Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

Lys	Xaa	Tyr	Xaa	Gln	Xaa	Xaa	Gly	Ile	Pro	Gln	Gly	Ser	Xaa	Leu	Ser
1				5					10					15	
Xaa Xaa Leu															

(2) INFORMATION FOR SEQ ID NO:637:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 Ala, Leu, Ile, Val, Pro, Phe,
 Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

Leu	Leu	Arg	Leu	Xaa	Asp	Asp	Xaa	Leu	Xaa	Ile	Thr
1				5						10	

(2) INFORMATION FOR SEQ ID NO:638:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3396
- (D) OTHER INFORMATION: /note= "hTRT-encoding sequence employing alternative codon distributions for E. coli (all genes)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

ATGCCGCGCG CGCCGCGCTG CCGCGCGGTG CGCAGCCTGC TGCGCAGCCA TTATCGCGAA	60
GTGCTGCCGC TGGCGACCTT TGTGCGCCGC CTGGGCCCGC AGGGCTGGCG CCTGGTGCAG	120
CGCGCGATC CGCGCGCGTT TCGCGCGCTG GTGGCGCAGT GCCTGGTGTG CGTGCCGTGG	180
GATGCGCGCC CGCCGCCGGC GGCGCCGAGC TTTGCCAGG TGAGCTGCCT GAAAGAACTG	240
GTGGCGCGCG TGCTGCAGCG CCTGTGCAGA CGCGCGCGGA AAAACGTGCT GGCCTTGGC	300
TTTGCCTGC TGGATGGCGC GCGCGCGGC CCGCCGGAAG CGTTTACAC CAGCGTGCAC	360
AGCTATCTGC CGAACACCGT GACCGATGCG CTGCGCGCA CGGGCGCGTG GGGCTGCTG	420
CTGCGCCGCG TGGCGATGA TGTGCTGGTG CATCTGCTGG CGCGCTGCAC GCTGTTGTG	480
CTGGTGGCGC CGAGCTGCAC GTATCAGGTG TGCGGCCCGC CGCTGTATCA GCTGGCGCG	540
GCGACCCAGG CGCGCCCGCC GCCGCATGCG AGCGCCCGC GCCGCCGCCT GGGCTGCGAA	600
CGCGCGTGGA ACCATAGCGT GCGCGAAGCG GGCGTGCCGC TGGGCCTGCC GGCGCCGGC	660
GCGCGCCGCC GCGGCGGCAG CGCGAGCCGC AGCCTGCCGC TGCGAAACG CCCGCGCCGC	720
GGCGCGGCCG CGGAACCGGA ACGCACCCCG GTGGGCCAGG GCAGCTGGC GCATCCGGC	780
CGCACCCGCG GCGCGAGCGA TCGCGGCTT TGCGTGGTGA GCGCCGCCGC CCCGGCGGAA	840
GAAGCGACCA GCCTGGAAGG CGCGCTGAGC GGCACCCGCC ATAGCCATCC GAGCGTGGC	900
CGCCAGCATC ATGCGGGCCC GCCGAGCACC AGCGCCGCCGC CGCGCCCGTG GGATACCCCG	960
TGCCCCGCCG TGTATGCGGA AACCAAACAT TTTCTGTATA GCAGCGCGA TAAAGAACAG	1020
CTGCGCCCGA GCTTCTGCT GAGCAGCCTG CGCCCGAGCC TGACCGGCCG GCGCCGCCCTG	1080
GTGGAAACCA TTTTCTGGG CAGCCGCCCG TGGATGCCGG GCACCCCGCG CGCCCTGCCG	1140
CGCCCTGCCGC AGCGCTATTG GCAGATGCCG CCGCTGTTTC TGGAACGTGCT GGGCAACCAT	1200
GCGCAGTGCC CGTATGGCGT GCTGCTGAAA ACCCATTGCC CGCTGCGCGC GGCGGTGACC	1260
CCGGCGGCCG GCGTGTGCGC GCGCGAAAAA CCGCAGGGCA GCGTGGCGGC GCCGGAAGAA	1320
GAAGATAACCG ATCCGCGCCG CCTGGTGCAG CTGCTGCGCC AGCATAGCAG CCCGTGGCAG	1380
GTGTATGGCT TTGTGCGCGC GTGCCTGCCG CGCCTGGTGC CGCCGGGCCT GTGGGGCAGC	1440
CGCCATAACG AACGCCGCTT TCTGCGAAC ACCAAAAAAT TTATTAGCCT GGGAAACCAT	1500
GCGAAACTGA GCCTGCAGGA ACTGACCTGG AAAATGAGCG TGCGCGATTG CGCGTGGCTG	1560
CGCCCGAGCC CGGGCGTGGG CTGCGTGCGC CGGGCGGAAC ATCGCCTGCG CGAAGAAATT	1620
CTGGCGAAAT TTCTGCATTG GCTGATGAGC GTGTATGTGG TGGAACGTGCT GCGCAGCTTT	1680
TTTTATGTGA CCGAAACAC CTTTCAGAAA AACCGCCTGT TTTTTATCG CAAAAGCGTG	1740
TGGAGCAAAC TGCAGAGCAT TGGCATTCGC CAGCATCTGA AACCGTGCAC GCTGCGCGAA	1800

CTGAGCGAAG CGGAAGTGC G	CCAGCATCG C	GAAGCGGCC CGGCGCTGCT GACCAGCCG	1860
CTGCGCTTTA TTCCGAAACC GGATGGCCTG CGCCCGATTG TGAACATGGA TTATGTGGT	G	GCGCGCGCA CCTTCGCCG CGAAAAACGC GCGGAACGCC TGACCAGCCG CGTGAAAGCG	1920
CTGTTTAGCG TGCTGAACTA TGAACGCC G	CGCCGCCCG GCCTGCTGGG CGCGAGCGTG	1980	
CTGGGCCTGG ATGATATTCA TCGCGCGTGG CGCACCTTG TGCTGCGCGT GCGCGCGCAG	G	GATCCGCCGC CGGAACTGTA TTTTGTGAAA GTGGATGTGA CCGGCGCGTA TGATACCATT	2040
CCGCAGGATC GCCTGACCGA AGTGATTGCG AGCATTATTA AACCGCAGAA CACCTATTGC	A	GTGCGCCGCT ATGCGGTGGT GCAGAAAGCG GCGCATGGCC ATGTGCGCAA AGCGTTAAA	2100
AGCCATGTGA GCACCCCTGAC CGATCTGCAG CCGTATATGC GCCAGTTGT GGCGCATCTG	T	CAGGAAACCA GCCCGCTGCG CGATGCGGTG GTGATTGAAC AGAGCAGCAG CCTGAACGAA	2160
CGGAGCAGCG GCCTGTTGA TGTGTTCTG CGCTTATGT GCCATCATGC GGTGCGCATT	A	CGCGGCAAAA GCTATGTGCA GTGCCAGGGC ATTCCGCAGG GCAGCATTCT GAGCACCTG	2220
CTGTGCAGCC TGTGCTATGG CGATATGGAA AACAAACTGT TTGCGGGCAT TCGCCGCGAT	C	GGCCTGCTGC TGCGCCTGGT GGATGATTCT CTGCTGGTGA CCCGCATCT GACCCATGCG	2280
AAAACCTTTC TGCGCACCCCT GGTGCGCGGC GTGCCGGAAT ATGGCTGCGT GGTGAACCTG	G	AAGTGCAGA GCGATTATAG CAGCTATGCG CGCACCAAGCA TTCGCGCGAG CCTGACCTT	2340
CGCAAAACCG TGGTGAACCTT TCCGGTGGAA GATGAAGCGC TGGGCGGCAC CGCGTTGTG	T	AACCGCGGCT TTAAAGCGGG CCGCAACATG CGCCGCAAAC TGTTGGCGT GCTGCGCCTG	2400
CAGATGCCGG CGCATGGCCT GTTCCCGTGG TGCGCCTGC TGCTGGATAC CCCCACCC	A	AAATGCCATA GCCTGTTCT GGATCTGCAG GTGAACAGCC TGCAGACCGT GTGCACCAAC	2460
ATTATAAAAA TTCTGCTGCT GCAGGCGTAT CGCTTTCATG CGTGCCTGCT GCAGCTGCCG	C	TTTCATCAGC AGGTGTGGAA AAACCCGACC TTTTTCTGC GCGTGATTAG CGATACCGCG	2520
AGCCTGTGCT ATAGCATTCT GAAAGCGAAA AACGCGGGCA TGAGCCTGGG CGCGAAAGGC	G	AACACTGACCC GCCATCGCGT GACCTATGTG CCGCTGCTGG GCAGCCTGCG CACCGCGCAG	2580
GCGGCGGGCC CGCTGCCGAG CGAACCGGTG CAGTGGCTGT GCCATCAGGC GTTCTGCTG	T	ACCCAGCTGA GCCGCAAAC ACCCTGACCG CGCTGGAAGC GGCGCGAAC	2640
AAACTGACCC GCCATCGCGT GACCTATGTG CCGCTGCTGG GCAGCCTGCG CACCGCGCAG	A	CCGGCGCTGC CGAGCGATT TAAAACCATT CTGGAT	3120
ACCCAGCTGA GCCGCAAAC ACCCTGACCG CGCTGGAAGC GGCGCGAAC	C	3300	
CCGGCGCTGC CGAGCGATT TAAAACCATT CTGGAT	G	3360	
CCGGCGCTGC CGAGCGATT TAAAACCATT CTGGAT	T	3396	

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3396
- (D) OTHER INFORMATION: /note= "hTRT-encoding sequence employing alternative codon distributions for enteric bacteria (high expressing genes)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

ATGCCGCGTG	CTCCGCGTTG	CCGTGCTGTT	CGTCCCTGC	TGCGTCCC	CTACCGTGAA	60
GTTCTGCCGC	TGGCTACCTT	CGTTCGTCGT	CTGGGTCCGC	AGGGTTGGCG	TCTGGTTCAG	120
CGTGGTGACC	CGGCTGCTTT	CCGTGCTCTG	GTTGCTCAGT	GCCTGGTTG	CGTCCGTGG	180
GACGCTCGTC	CGCCGCCGGC	TGCTCCGTCC	TTCCGTCAGG	TTTCCTGCCT	GAAAGAACTG	240
GTTGCTCGTG	TTCTGCAGCG	TCTGTGCGAA	CGTGGTGCTA	AAAACGTTCT	GGCTTTCGGT	300
TTCGCTCTGC	TGGACGGTGC	TCGTGGTGGT	CCGCCGGAAAG	CTTCACCAAC	CTCCGTTCGT	360
TCCCTACCTGC	CGAACACCGT	TACCGACGCT	CTGCGTGGTT	CCGGTGCTTG	GGGTCTGCTG	420
CTGCGTCGTG	TTGGTGACGA	CGTTCTGGTT	CACCTGCTGG	CTCGTTCCGC	TCTGTTCGTT	480
CTGGTTGCTC	CGTCCTGCC	TTACCAGGTT	TGCGGTCCGC	CGCTGTACCA	GCTGGGTGCT	540
GCTACCCAGG	CTCGTCCGCC	GCCGCACGCT	TCCGGTCCGC	GTCGTCGTCT	GGTTGCGAA	600
CGTGCTTGGA	ACCACTCCGT	TCGTGAAGCT	GGTGGTCCGC	TGGGTCTGCC	GGCTCCGGGT	660
GCTCGTCGTC	GTGGTGGTTC	CGCTTCCCGT	TCCCTGCCGC	TGCCGAAACG	TCCCGTCGT	720
GGTGCTGCTC	CGGAACCGGA	ACGTACCCCCG	GTTGGTCAGG	GTTCCTGGGC	TCACCCGGGT	780
CGTACCCGTG	GTCCGTCCGA	CCGTGGTTTC	TGCGTTGTTT	CCCCGGCTCG	TCCGGCTGAA	840
GAAGCTACCT	CCCTGGAAGG	TGCTCTGTCC	GGTACCCGTC	ACTCCCACCC	GTCCGTTGGT	900
CGTCAGCAC	ACGCTGGTCC	GCCGTCCACC	TCCCGTCCGC	CGCGTCCGTG	GGACACCCCCG	960
TGCCCGCCGG	TTTACGCTGA	AACCAAACAC	TTCCTGTACT	CCTCCGGTGA	CAAAGAACAG	1020
CTGCGTCGT	CCTTCCTGCT	GTCCTCCCTG	CGTCCGTCCC	TGACCGGTGC	TCGTCGTCTG	1080
GTTGAAACCA	TCTTCCTGGG	TTCCCGTCCG	TGGATGCCGG	GTACCCCGCG	TCGTCTGCCG	1140
CGTCTGCCGC	AGCGTTACTG	GCAGATGCGT	CCGCTGTTCC	TGGAAC TGCT	GGGTAACCAC	1200

GCTCAGTGCC CGTACGGTGT TCTGCTGAAA ACCCACTGCC CGCTGCGTGC TGCTGTTACC	1260
CCGGCTGCTG GTGTTGCGC TCGTGAAAAA CCGCAGGGTT CCGTTGCTGC TCCGGAAGAA	1320
GAAGACACCG ACCCGCGTCG TCTGGTTCAAG CTGCTGCGTC AGCACTCCTC CCCGTGGCAG	1380
GTTTACGGTT TCGTTCGTGC TTGCCTGCGT CGTCTGGTTC CGCCGGGTCT GTGGGGTTCC	1440
CGTCACAACG AACGTCGTTT CCTGCGTAAC ACCAAAAAAAT TCATCTCCCT GGGTAAACAC	1500
GCTAAACTGT CCCTGCAGGA ACTGACCTGG AAAATGTCCG TTCGTGACTG CGCTTGGCTG	1560
CGTCGTTCCC CGGGTGTGG TTGCCTCCG GCTGCTGAAC ACCGTCTGCG TGAAGAAATC	1620
CTGGCTAAAT TCCTGCACTG GCTGATGTCC GTTACGTTG TTGAACTGCT GCCTCCCTTC	1680
TTCTACGTTA CCGAAACAC CTTCCAGAAA AACCGTCTGT TCTTCTACCG TAAATCCGTT	1740
TGGTCCAAAC TGCAGTCCAT CGGTATCCGT CAGCACCTGA AACGTGTTCA GCTGCGTGAA	1800
CTGTCCGAAG CTGAAGTTCG TCAGCACCGT GAAGCTCGTC CGGCTCTGCT GACCTCCCGT	1860
CTGCCTTCA TCCCCAAACC GGACGGTCTG CGTCCGATCG TTAACATGGA CTACGTTGTT	1920
GGTGCTCGTA CCTTCCGTCG TGAAAAACGT GCTGAACGTC TGACCTCCCG TGTTAAAGCT	1980
CTGTTCTCCG TTCTGAACTA CGAACGTGCT CGTCGTCCGG GTCTGCTGGG TGCTTCCGTT	2040
CTGGGTCTGG ACGACATCCA CGTGCTTGG CGTACCTTCG TTCTGCGTGT TCGTGCTCAG	2100
GACCCGCCGC CGGAACGTGA CTTCGTTAA GTTGACGTTA CCGGTGCTTA CGACACCATC	2160
CCGCAGGACC GTCTGACCGA AGTTATCGCT TCCATCATCA AACCGCAGAA CACCTACTGC	2220
GTTCGTCGTT ACGCTGTTGT TCAGAAAGCT GCTCACGGTC ACGTTCGTAA AGCTTCAAA	2280
TCCCCACGTTT CCACCCGTGAC CGACCTGCAG CCGTACATGC GTCAGTTCGT TGCTCACCTG	2340
CAGGAAACCT CCCCCGCTGCG TGACGCTGTT GTTATCGAAC AGTCCTCCTC CCTGAACGAA	2400
GCTTCCTCCG GTCTGTTCGA CGTTTCCTG CGTTTCATGT GCCACCACGC TGTCGTATC	2460
CGTGGTAAAT CCTACGTTCA GTGCCAGGGT ATCCCGCAGG GTTCCATCCT GTCCACCCCTG	2520
CTGTGCTCCC TGTGCTACGG TGACATGGAA AACAAACTGT TCGCTGGTAT CCGTCGTGAC	2580
GGTCTGCTGC TGCCTGCTGGT TGACGACTTC CTGCTGGTTA CCCCCGACCT GACCCACGCT	2640
AAAACCTTCC TGCCTGACCCCT GGTCGTTGGT GTTCCGGAAT ACGGTTGCGT TGTTAACCTG	2700
CGTAAAACCG TTGTTAACTT CCCGGTTGAA GACGAAGCTC TGGGTGGTAC CGCTTTCGTT	2760
CAGATGCCGG CTCACGGTCT GTTCCCGTGG TGCGGTCTGC TGCTGGACAC CCGTACCCCTG	2820
GAAGTTCACT CCGACTACTC CTCCTACGCT CGTACCTCCA TCCGTGCTTC CCTGACCTTC	2880
AACCGTGGTT TCAAAGCTGG TCGTAACATG CGTCGTAAAC TGTTCGGTGT TCTGCGTCTG	2940
AAATGCCACT CCCTGTTCCCT GGACCTGCAG GTTAACTCCC TGCAGACCGT TTGCACCAAC	3000
ATCTACAAAAA TCCTGCTGCT GCAGGCTTAC CGTTCCACG CTTGCGTTCT GCAGCTGCCG	3060

TTCCACCAGC AGGTTGGAA AAACCCGACC TTCTTCCTGC GTGTTATCTC CGACACCGCT	3120
TCCCTGTGCT ACTCCATCCT GAAAGCTAAA AACGCTGGTA TGTCCCTGGG TGCTAAAGGT	3180
GCTGCTGGTC CGCTGCCGTC CGAAGCTGTT CAGTGGCTGT GCCACCAGGC TTTCCCTGCTG	3240
AAACTGACCC GTCACCGTGT TACCTACGTT CCGCTGCTGG GTTCCCTGCG TACCGCTCAG	3300
ACCCAGCTGT CCCGTAAACT GCCGGGTACC ACCCTGACCG CTCTGGAAGC TGCTGCTAAC	3360
CCGGCTCTGC CGTCCGACTT CAAAACCATC CTGGAC	3396

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3396
- (D) OTHER INFORMATION: /note= "hTRT-encoding sequence employing alternative codon distributions for yeast (all genes)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

ATGCCAAGAG CTCCAAGATG TAGAGCTGTT AGATCTTGT TGAGATCTCA TTATAGAGAA	60
GTTTGCCAT TGGCTACTTT TGTAGAAGA TTGGTCCAC AAGGTTGGAG ATTGGTCAA	120
AGAGGTGATC CAGCTGCTTT TAGAGCTTTG GTTGCTCAAT GTTGGTTTG TGTCCATGG	180
GATGCTAGAC CACCACCAAGC TGCTCCATCT TTTAGACAAG TTTCTTGTAA GAAAGAATTG	240
GTTGCTAGAG TTTGCAAAG ATTGTGTGAA AGAGGTGCTA AAAATGTTT GGCTTTGGT	300
TTTGCTTTGT TGGATGGTGC TAGAGGTGGT CCACCAAGAG CTTTTACTAC TTCTGTTAGA	360
TCTTATTGCAAAATACTGT TACTGATGCT TTGAGAGGTT CTGGTGCTTG GGGTTTGTG	420
TTGAGAAGAG TTGGTGATGA TGTTTGGTT CATTGTTGG CTAGATGTGC TTTGTTGTT	480
TTGGTTGCTC CATCTTGTGC TTATCAAGTT TGTGGTCCAC CATTGTATCA ATTGGGTGCT	540
GCTACTCAAG CTAGACCACC ACCACATGCT TCTGGTCCAA GAAGAAGATT GGGTTGTGAA	600
AGAGCTTGGA ATCATTCTGT TAGAGAAGCT GGTGGTCCAT TGGGTTGCC AGCTCCAGGT	660
GCTAGAAGAA GAGGTGGTTC TGCTTCTAGA TCTTGCCAT TGCCAAAAAG ACCAAGAAGA	720
GGTGCTGCTC CAGAACCAAGA AAGAACTCCA GTTGGTCAAG GTTCTTGGC TCATCCAGGT	780
AGAACTAGAG GTCCCATCTGA TAGAGGTTT TGTGTTGTT CTCCAGCTAG ACCAGCTGAA	840

GAAGCTACTT CTTTGGAAAGG TGCTTTGTCT GGTACTAGAC ATTCTCATCC ATCTGTTGGT	900
AGACAAACATC ATGCTGGTCC ACCATCTACT TCTAGACCAC CAAGACCATG GGATACTCCA	960
TGTCCACCAG TTTATGCTGA AACTAAACAT TTTTTGTATT CTTCTGGTGA TAAAGAACAA	1020
TTGAGACCAC CTTTTTGTT GTCTTCTTG AGACCACCTT TGACTGGTGC TAGAAGATTG	1080
GTTGAAACTA TTTTTTGGG TTCTAGACCA TGGATGCCAG GTACTCCAAG AAGATTGCCA	1140
AGATTGCCAC AAAGATATTG GCAAATGAGA CCATTGTTT TGGAATTGTT GGGTAATCAT	1200
GCTCAATGTC CATATGGTGT TTTGTTGAAA ACTCATTGTC CATTGAGAGC TGCTGTTACT	1260
CCAGCTGCTG GTGTTGTGC TAGAGAAAAA CCACAAGGTT CTGTTGCTGC TCCAGAAGAA	1320
GAAGATACTG ATCCAAGAAG ATTGGTTCAA TTGTTGAGAC AACATTCTTC TCCATGGCAA	1380
GTTTATGGTT TTGTTAGAGC TTGTTGAGA AGATGGTTC CACCAGGTT GTGGGGTTCT	1440
AGACATAATG AAAGAAGATT TTTGAGAAAT ACTAAAAAAT TTATTTCTT GGGTAAACAT	1500
GCTAAATTGT CTTTGCAAGA ATTGACTTGG AAAATGTCTG TTAGAGATTG TGCTTGGTTG	1560
AGAAGATCTC CAGGTGTTGG TTGTGTTCCA GCTGCTGAAC ATAGATTGAG AGAAGAAATT	1620
TTGGCTAAAT TTTTGCATTG GTTGATGTCT GTTTATGTTG TTGAATTGTT GAGATCTTT	1680
TTTTATGTTA CTGAAACTAC TTTCAAAAAA AATAGATTGT TTTTTATAG AAAATCTGTT	1740
TGGTCTAAAT TGCAATCTAT TGGTATTAGA CAACATTGA AAAGAGTTCA ATTGAGAGAA	1800
TTGCTGAAAG CTGAAGTTAG ACAACATAGA GAAGCTAGAC CAGCTTGTT GACTTCTAGA	1860
TTGAGATTAA TTCCAAAACC AGATGGTTG AGACCAATTG TTAATATGGA TTATGTTGTT	1920
GGTGCTAGAA CTTTAGAAG AGAAAAAAGA GCTGAAAGAT TGACTTCTAG AGTTAAAGCT	1980
TTGTTTCTG TTTGAAATTA TGAAAGAGCT AGAAGACCAG GTTTGTTGGG TGCTTCTGTT	2040
TTGGGTTGG ATGATATTCA TAGAGCTTGG AGAACCTTG TTTGAGAGT TAGAGCTCAA	2100
GATCCACCAC CAGAATTGTA TTTGTTAAA GTTGATGTTA CTGGTGCTTA TGATACTATT	2160
CCACAAGATA GATTGACTGA AGTTATTGCT TCTATTATTA AACCACAAAA TACTTATTGT	2220
GTAGAAGAT ATGCTGTTGT TCAAAAAGCT GCTCATGGTC ATGTTAGAAA AGCTTTAAA	2280
TCTCATGTTT CTACTTGAC TGATTTGCAA CCATATATGA GACAATTGTT TGCTCATTG	2340
CAAGAAACTT CTCCATTGAG AGATGCTGTT GTTATTGAAC AATCTTCTTC TTTGAATGAA	2400
GCTTCTTCTG GTTTGTTGA TGTTTTTG AGATTTATGT GTCATCATGC TGTTAGAATT	2460
AGAGGTAAAT CTTATGTTCA ATGTCAAGGT ATTCCACAAG GTTCTATTGTT GTCTACTTTG	2520
TTGTTGTTCTT TGTGTTATGG TGATATGGAA AATAAATTGT TTGCTGGTAT TAGAAGAGAT	2580
GGTTGTTGTT TGAGATTGGT TGATGATTGTT TTGTTGGTTA CTCCACATTG GACTCATGCT	2640
AAAACTTTT TGAGAACTTT GGTTAGAGGT GTTCCAGAAT ATGGTTGTGT TGTTAATTG	2700

AGAAAAACTG TTGTTAATT TCCAGTTGAA GATGAAGCTT TGGGTGGTAC TGCTTTGTT	2760
CAAATGCCAG CTCATGGTTT GTTCCATGG TGTGGTTGT TGTTGGATAC TAGAACTTTG	2820
GAAGTTCAAT CTGATTATTC TTCTTATGCT AGAACTTCTA TTAGAGCTTC TTTGACTTT	2880
AATAGAGGTT TTAAAGCTGG TAGAAATATG AGAAGAAAAT TGTTGGTGT TTTGAGATTG	2940
AAATGTCATT CTTTGTTTT GGATTGCAA GTTAATTCTT TGCAAACGTG TTGTACTAAT	3000
ATTTATAAAA TTTTGTGTT GCAAGCTTAT AGATTTCATG CTTGTGTTT GCAATTGCCA	3060
TTTCATCAAC AAGTTGGAA AAATCCAAT TTTTTTGAGAGTTATTG TGATACTGCT	3120
TCTTGTGTT ATTCTATTT GAAAGCTAAA AATGCTGGTA TGTCTTGAG TGCTAAAGGT	3180
GCTGCTGGTC CATTGCCATC TGAAGCTGTT CAATGGTTGT GTCATCAAGC TTTTTGTTG	3240
AAATTGACTA GACATAGAGT TACTTATGTT CCATTGTTGG GTTCTTGAG AACTGCTCAA	3300
ACTCAATTGT CTAGAAAATT GCCAGGTACT ACTTTGACTG CTTTGGAAAGC TGCTGCTAAT	3360
CCAGCTTGC CATCTGATT TAAAACATT TTGGAT	3396

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3396
- (D) OTHER INFORMATION: /note= "hTRT-encoding sequence employing alternative codon distributions for yeast (high expressing genes)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

ATGCCAAGAG CTCCAAGATG TAGAGCTGTT AGATCTTGT TGAGATCTCA CTACAGAGAA	60
GTTCAGCCAT TGGCTACTTT CGTTAGAAGA TTGGGTCCAC AAGGTTGGAG ATTGGTTCAA	120
AGAGGTGACC CAGCTGCTTT CAGAGCTTTG GTTGCTCAAT GTTGGTTTG TGTTCCATGG	180
GACGCTAGAC CACCACCAAGC TGCTCCATCT TTCAGACAAG TTTCTTGTGTT GAAGGAATTG	240
GTTGCTAGAG TTTTGCAAAAG ATTGTGTGAA AGAGGTGCTA AGAACGTTT GGCTTCGGT	300
TTCGCTTTGT TGGACGGTGC TAGAGGTGGT CCACCAAGAAG CTTTCACTAC TTCTGTTAGA	360
TCTTACTTGC CAAACACTGT TACTGACGCT TTGAGAGGTT CTGGTGCTTG GGGTTGTTG	420
TTGAGAAGAG TTGGTGACGA CGTTTGGTT CACTGTTGG CTAGATGTGC TTTGTTCGTT	480

TTGGTTGCTC CATCTTGTGC TTACCAAGTT TGTGGTCCAC CATTGTACCA ATTGGGTGCT	540
GCTACTCAAG CTAGACCACC ACCACACGCT TCTGGTCCAA GAAGAAGATT GGGTTGTGAA	600
AGAGCTTGGGA ACCACTCTGT TAGAGAAGCT GGTGTTCCAT TGGGTTGCC AGCTCCAGGT	660
GCTAGAAGAA GAGGTGGTTC TGCTTCTAGA TCTTGCCAT TGCCAAAGAG ACCAAGAAGA	720
GGTGCTGCTC CAGAACCGAGA AAGAACTCCA GTTGGTCAAG GTTCTGGGC TCACCCAGGT	780
AGAACTAGAG GTCCATCTGA CAGAGGTTTC TGTGTTGTTT CTCCAGCTAG ACCAGCTGAA	840
GAAGCTACTT CTTTGGAAAGG TGCTTGCTCT GGTACTAGAC ACTCTCACCC ATCTGTTGGT	900
AGACAACACC ACGCTGGTCC ACCATCTACT TCTAGACCAC CAAGACCATG GGACACTCCA	960
TGTCCACCAG TTTACGCTGA AACTAAGCAC TTCTTGTACT CTTCTGGTGA CAAGGAACAA	1020
TTGAGACCAT CTTTCTTGTT GTCTTCTTG AGACCATCTT TGACTGGTGC TAGAAGATTG	1080
GTGAAACTA TTTTCTTGGG TTCTAGACCA TGGATGCCAG GTACTCCAAG AAGATTGCCA	1140
AGATTGCCAC AAAGATACTG GCATAATGAGA CCATTGTTCT TGGATTGTT GGGTAACCAC	1200
GCTCAATGTC CATAACGGTGT TTTGTTGAAG ACTCACTGTC CATTGAGAGC TGCTGTTACT	1260
CCAGCTGCTG GTGTTGTGC TAGAGAAAAG CCACAAGGTT CTGTTGCTGC TCCAGAAGAA	1320
GAAGACACTG ACCCAAGAAG ATTGGTTCAA TTGTTGAGAC AACACTCTTC TCCATGGCAA	1380
GTTTACGGTT TCGTTAGAGC TTGTTGAGA AGATGGTTC CACCAGGTTT GTGGGGTTCT	1440
AGACACAAACG AAAGAAGATT CTTGAGAAAC ACTAAGAAAGT TCATTCTTT GGGTAAGCAC	1500
GCTAAGTTGT CTTGCAAGA ATTGACTTGG AAGATGTCTG TTAGAGACTG TGCTTGGTTG	1560
AGAAGATCTC CAGGTGTTGG TTGTGTTCCA GCTGCTGAAC ACAGATTGAG AGAAGAAATT	1620
TTGGCTAAGT TCTTGCAC TGTTGATGTCT GTTTACGTTG TTGAATTGTT GAGATCTTTC	1680
TTCTACGTTA CTGAAACTAC TTTCCAAAAG AACAGATTGT TCTTCTACAG AAAGTCTGTT	1740
TGGTCTAAGT TGCAATCTAT TGGTATTAGA CAACACTTGA AGAGAGTTCA ATTGAGAGAA	1800
TTGTCTGAAG CTGAAGTTAG ACAACACAGA GAAGCTAGAC CAGCTTGTT GACTTCTAGA	1860
TTGAGATTCA TTCCAAAGCC AGACGGTTG AGACCAATTG TTAACATGGA CTACGTTGTT	1920
GGTGCTAGAA CTTTCAGAAG AGAAAAGAGA GCTGAAAGAT TGACTTCTAG AGTTAAGGCT	1980
TTGTTCTCTG TTTTGAACTA CGAAAGAGCT AGAAGACCAG GTTTGTTGGG TGCTTCTGTT	2040
TTGGGTTTGG ACGACATTCA CAGAGCTTGG AGAACCTTCG TTTTGAGAGT TAGAGCTCAA	2100
GACCCACCAC CAGAATTGTA CTTCGTTAAG GTTGACGTTA CTGGTGCTTA CGACACTATT	2160
CCACAAGACA GATTGACTGA AGTTATTGCT TCTATTATTA AGCCACAAAA CACTTACTGT	2220
GTTAGAAGAT ACGCTGTTGT TCAAAAGGCT GCTCACGGTC ACGTTAGAAA GGCTTCAAG	2280
TCTCACGTTT CTACTTGAC TGACTTGCAA CCATACATGA GACAATTCGT TGCTCACTTG	2340

CAAGAAACTT CTCCATTGAG AGACGCTGTT GTTATTGAAC AATCTTCTTC TTTGAACGAA	2400
GCTTCTTCTG GTTTGTTCGA CGTTTCTTG AGATTCATGT GTCACCACGC TGTTAGAATT	2460
AGAGGTAAGT CTTACGTTCA ATGTCAAGGT ATTCCACAAG GTTCTATTT GTCTACTTTG	2520
TTGTGTTCTT TGTGTTACGG TGACATGGAA AACAAAGTTGT TCGCTGGTAT TAGAAGAGAC	2580
GGTTTGTGTT TGAGATTGGT TGACGACTTC TTGTTGGTTA CTCCACACTT GACTCACGCT	2640
AAGACTTTCT TGAGAACTTT GGTTAGAGGT GTTCCAGAAT ACGGTTGTGT TGTTAAC TTG	2700
AGAAAGACTG TTGTTAAC TTCCCAGTTGAA GACGAAGCTT TGGGTGGTAC TGCTTTCGTT	2760
CAAATGCCAG CTCACGGTTT GTTCCCAGTGG TGTGGTTGT TGTTGGACAC TAGAAC TTG	2820
GAAGTTCAAT CTGACTACTC TTCTTACGCT AGAAC TTCTA TTAGAGCTTC TTTGACTTT	2880
AACAGAGGTT TCAAGGCTGG TAGAAACATG AGAAGAAAGT TGTTGGTGT TTTGAGATTG	2940
AAGTGTCACT CTTTGTCTT GGACTTGCAA GTTAACTCTT TGCAAACTGT TTGACTAAC	3000
ATTTACAAGA TTTTGTGTT GCAAGCTTAC AGATCCACG CTTGTGTTTG GCAATTGCCA	3060
TTCCACCAAC AAGTTGGAA GAACCCA ACT TTCTTCTTGA GAGTTATTTC TGACACTGCT	3120
TCTTGTTGTT ACTCTATTTT GAAGGCTAAG AACGCTGGTA TGTCTTG G TGCTAAGGGT	3180
GCTGCTGGTC CATTGCCATC TGAAGCTGTT CAATGGTTGT GTCACCAAGC TTTCTTGTG	3240
AAGTTGACTA GACACAGAGT TACTTACGTT CCATTGTTGG GTTCTTGAG AACTGCTCAA	3300
ACTCAATTGT CTAGAAAGTT GCCAGGTACT ACTTTGACTG CTTTGGAAAGC TGCTGCTAAC	3360
CCAGCTTGC CATCTGACTT CAAGACTATT TTGGAC	3396

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3396
- (D) OTHER INFORMATION: /note= ""generic" hTRT protein encoding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

ATGCCACGTG CCCCACGTTG TCGTGCCGTT CGTTCTTGT TGCCTCTCA CTACCGTGA	60
GTGTTGCCAT TGGCCACCTT CGTCGTCGT TTGGTCCAC AAGGTTGGCG TTTGGTTCAA	120
CGTGGTGATC CAGCCGCCTT CGTGCCTTG GTTGCCAAT GTTGGTTG TGTTCCATGG	180

GATGCCCGTC CACCACCAAGC CGCCCCATCT TTCCGTCAAG TTTCTTGTGTT GAAAGAATTG	240
GTTGCCCGTG TTTTGCACAGC TTTGTGTGAA CGTGGTGCCTT AAAACGTTT GGCCTTCGGT	300
TTCGCCTTGT TGGATGGTGC CCGTGGTGGT CCACCAGAAG CCTTCACCCAC CTCTGTTCGT	360
TCTTACTTGC CAAACACCGT TACCGATGCC TTGGTGGTCTG CTGGTGCCTG GGGTTTGTG	420
TTGCGTCGTG TTGGTGATGA TGTTTGGTT CACTTGTGG CCCGTTGTGC CTTGTTCGTT	480
TTGGTTGCCCATCTTGTGC CTACCAAGTT TGTGGTCCAC CATTGTACCA ATTGGGTGCC	540
GCCACCCAAG CCCGTCCACC ACCACACGCC TCTGGTCCAC GTGTCGTTT GGGTTGTGAA	600
CGTGCCTGGA ACCACTCTGT TCGTGAAGCC GGTGTTCCAT TGGGTTGCC AGCCCCAGGT	660
GCCC GTGGTGGTTC TGCCTCTCGT TCTTGCCAT TGCCAAAACG TCCACGTCGT	720
GGTGCCTGCC CAGAACCAAGA ACGTACCCCCA GTTGGTCAAG GTTCTTGGC CCACCCAGGT	780
CGTACCCGTG GTCCATCTGA TCGTGGTTTC TGTGTTGTTT CTCCAGCCCC TCCAGCCGAA	840
GAAGCCACCT CTTTGGAAAGG TGCCTTGCT GGTACCCGTC ACTCTCACCC ATCTGTTGGT	900
CGTCAACACC ACGCCGGTCC ACCATCTACC TCTCGTCCAC CACGTCCATG GGATACCCCCA	960
TGTCCACCAG TTTACGCCGA AACCAAACAC TTCTTGTACT CTTCTGGTGA TAAAGAACAA	1020
TTGCGTCCAT CTTTCTTGTGTT GTCTTCTTGT CGTCCATCTT TGACCGGTGC CCGTCGTTTG	1080
GTGAAACCA TTTTCTTGGG TTCTCGTCCA TGGATGCCAG GTACCCACG TCAGTTGCCA	1140
CGTTGCCAC AACGTTACTG GCAAATGCGT CCATTGTTCT TGGATTGTT GGGTAACCAC	1200
GCCCAATGTC CATA CGGTGT TTTGTTGAAA ACCCACTGTC CATTGCGTGC CGCCGTTACC	1260
CCAGCCGCCG GTGTTGTGC CCGTGAAAAA CCACAAGGTT CTGTTGCCGC CCCAGAACAA	1320
GAAGATAACCG ATCCACGTCG TTTGGTTCAA TTGTTGCGTC AACACTCTTC TCCATGGCAA	1380
GTTCACGGTT TCGTTCGTGC CTGTTGCCGT CGTTGGTTC CACCAGGTTT GTGGGGTTCT	1440
CGTCACAACG AACGTCGTTT CTTGCGTAAC ACCAAAAAAT TCATTTCTT GGGTAAACAC	1500
GCCAAATTGT CTTTGCAGA ATTGACCTGG AAAATGTCTG TTGATGATTG TGCTGGTTG	1560
CGTCGTTCTC CAGGTGTTGG TTGTTGCCA GCCGCCGAAC ACCGTTGCG TGAAGAAATT	1620
TTGGCCAAAT TCTTGCAC TGTTGATGTCT GTTACGTTG TTGAATTGTT CGTTCTTTC	1680
TTCTACGTTA CCGAAACAC CTTCCAAAAA AACCGTTGT TCTTCTACCG TAAATCTGTT	1740
TGGTCTAAAT TGCAATCTAT TGGTATTGCGT CAACACTTGA AACGTGTTCA ATTGCGTGAA	1800
TTGTCGAAG CCGAAGTTCG TCAACACCGT GAAGCCCGTC CAGCCTTGT GACCTCTCGT	1860
TTGCGTTCA TTCCAAAACC AGATGGTTTG CGTCCAATTG TTAACATGGA TTACGTTGTT	1920
GGTGCCTGCC TA CCTTCCGTCG TGAAAAACGT GCCGAACGTT TGACCTCTCG TGTTAAAGCC	1980
TTGTTCTCTG TTTTGAACTA CGAACGTGCC CGTCGTCAG GTTGTGTTGG TGCTCTGTT	2040

TTGGGTTTGG ATGATATTCA CCGTGCCTGG CGTACCTTCG TTTTGCCTGT TCGTGCCCAA	2100
GATCCACCAC CAGAATTGTA CTTCGTTAAA GTTGATGTTA CCGGTGCCTA CGATACCATT	2160
CCACAAGATC GTTTGACCGA AGTTATTGCC TCTATTATTA AACACAAAAA CACCTACTGT	2220
GTTCGTCGTT ACGCCGTTGT TCAAAAAGCC GCCCACGGTC ACGTTCGTAA AGCCTCAAA	2280
TCTCACGTTT CTACCTTGAC CGATTTGCAA CCATACATGC GTCAATTGCT TGCCCACTTG	2340
CAAGAACCT CTCCATTGCG TGATGCCGTT GTTATTGAAC AATCTTCTTC TTTGAACGAA	2400
GCCTCTTCTG GTTTGTTCGA TGTTTCTTG CGTTTCATGT GTCACCACGC CGTCGTATT	2460
.CGTGGTAAAT CTTACGTTCA ATGTCAAGGT ATTCCACAAG GTTCTATTT GTCTACCTTG	2520
TTGTGTTCTT TGTGTTACGG TGATATGGAA AACAAATTGT TCGCCGGTAT TCGTCGTGAT	2580
GGTTTGTGTT TGCGTTGGT TGATGATTTC TTGTTGGTTA CCCCCACACTT GACCCACGCC	2640
AAAACCTTCT TGCACCGTT GGTCGTGGT GTTCCAGAAT ACGGTTGTGT TGTAACTTG	2700
CGTAAAACCG TTGTTAACTT CCCAGTTGAA GATGAAGCCT TGGGTGGTAC CGCCTTCGTT	2760
CAAATGCCAG CCCACGGTTT GTTCCCATGG TGTGGTTGT TGTTGGATAC CCGTACCTTG	2820
GAAGTTCAAT CTGATTACTC TTCTTACGCC CGTACCTCTA TTCGTGCCTC TTTGACCTTC	2880
AACCGTGGTT TCAAAGCCGG TCGTAACATG CGTCGTAAAT TGTTGGTGT TTTGCCTTG	2940
AAATGTCACT CTTTGTCTT GGATTTGCAA GTTAACTCTT TGCAAACCGT TTGTACCAAC	3000
ATTTACAAAA TTTTGTGTT GCAAGCCTAC CGTTCCACG CCTGTGTTTT GCAATTGCCA	3060
TTCCACCAAC AAGTTGGAA AAACCCAACC TTCTTCTTGC GTGTTATTTC TGATACCGCC	3120
TCTTGTTACTCTT GAAAGCCAAA AACGCCGGTA TGTCTTGGG TGCAAAGGT	3180
GCCGCCGGTC CATTGCCATC TGAAGCCGTT CAATGGTTGT GTCACCAAGC CTTCTGTTG	3240
AAATTGACCC GTCACCGTGT TACCTACGTT CCATTGTTGG GTTCTTGC G TACCGCCCAA	3300
ACCCAATTGT CTCGTAAATT GCCAGGTACC ACCTTGACCG CCTTGGAAAGC CGCCGCCAAC	3360
CCAGCCTTGC CATCTGATTT CAAAACCATT TTGGAT	3396

(2) INFORMATION FOR SEQ ID NO:643:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: /note= "oligonucleotide 1B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

CCAGCGGCAG AACTTCGCGA TAGTGGGAAC GCAGCAGGGA ACGAACAGCA CGGCAACGCG	60
GAGCACGCCG CATATGGTCG ACTCTAGAGC TCCCCCGGTGC	100

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 1T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

GCACGCGGGA GCTCTAGAGT CGACCATATG CCGCGTGCTC CGCGTTGCCG TGCTGTTCGT	60
TCCCTGCTGC GTTCCCACTA TCGCGAAGTT	90

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 2B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

GGCACTGAGC AACCAAGAGCA CGGAAAGCAG CCGGGTCACC ACGCTGAACC AGACGCCAAC	60
CCTGCGGGCC CAGACGACGA ACGAAGGTAG	90

(2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 2T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

CTGCCGCTGG CTACCTTCGT TCGTCGTCTG GGCCCGCAGG GTTGGCGTCT GGTCAGCGT	60
GGTGACCCGG CTGCTTCCG TGCTCTGGTT	90

(2) INFORMATION FOR SEQ ID NO:647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 3B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

GAACACGAGC AACCAGTTCT TTCAGGCAGG AAACCTGACG GAAGGACCGA GCAGCCGGCG	60
CGGGACGAGC GTCCCACCGA ACGCAAACCA	90

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 3T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

GCTCAGTGCC TGGTTGCGT TCCGTGGAC GCTCGTCCGC CGCCGGCTGC TCCGTCCTTC	60
CGTCAGGTTT CCTGCCTGAA AGAACTGGTT	90

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 4B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

ATGCTTCCGG CGGACCACCA CGAGCACCGT CCAGCAGAGC GAAACCGAAA GCCAGAACGT	60
TTTAGCACC ACGTCGCAC AGACGCTGCA	90

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 4T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

GCTCGTGTTC TGCAGCGTCT GTGCGAACGT GGTGCTAAAA ACGTTCTGGC TTTCGGTTTC	60
GCTCTGCTGG ACGGTGCTCG TGGTGGTCCG	90

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 5B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

CAACACGACG CAGCAGCAGA CCCCAAGCAC CGGAACCACG CAGAGCGTCG GTAACGGTGT	60
TCGGCAGGTA GGAACGAACG GAGGTGGTGA	90

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 5T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

CCGGAAGCAT TCACCAACCTC CGTTCGTTCC TACCTGCCGA ACACCGTTAC CGACGCTCTG	60
CGTGGTTCCG GTGCTTGGGG TCTGCTGCTG	90

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 6B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

GCGGCGGACC ACAAACCTGG TAAGCGCAGG ACGGAGCAAC CAGAACGAAC AGAGCGAAC	60
GAGCCAGCAG GTGAACCAGA ACGTCGTAC	90

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 6T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

CGTCGTGTTG GTGACGACGT TCTGGTCAC CTGCTGGCTC GTTGCGCTCT GTTCGTTCTG	60
GTTGCTCCGT CCTGCGCTTA CCAGGTTTGT	90

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 7B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

GGTTCCAAGC ACGTCGCAA CCCAGACGAC GACGCGGACC GGAAGCGTGC GGCGGCGGAC	60
GAGCCTGGGT AGCAGCACCC AGCTGGTACA	90

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 7T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

GGTCCGCCGC TGTACCAGCT GGGTGCTGCT ACCCAGGCTC GTCCGCCGCC GCACGCTTCC	60
GGTCCGCCGTGTC GTCGCTCTGGG TTGCGAACGT	90

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 8B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

GCAGCGGGCAG GGAACGGGAA GCGGAACCAAC CACGACGACG AGCACCCCGGA GCCGGCAGAC	60
CCAGCGGAAC ACCAGCTTCA CGAACGGAGT	90

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 8T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

GCTTGGAACCC	ACTCCGTTCG	TGAAGCTGGT	GTTCCGCTGG	GTCTGCCGGC	TCCGGGTGCT	60
CGTCGTCGTG	GTGGTTCCGC	TTCCCGTTCC				90

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 9B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

GACCACGGGT	ACGACCCGGG	TGAGCCCAGG	AACCTGACC	AACCAGGGTA	CGTTCCGGTT	60
CCGGAGCAGC	ACCACGACGC	GGACGTTTCG				90

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 9T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

CTGCCGCTGC	CGAACGTCC	GCGTCGTGGT	GCTGCTCCGG	AACCGGAACG	TACCCCGGTT	60
GGTCAGGGTT	CCTGGGCTCA	CCCGGGTCGT				90

(2) INFORMATION FOR SEQ ID NO:661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 10B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

AGTGACGGGT GCCGGACAGA GCACCTCCA GGGAGGTTAGC TTCTTCAGCC GGACGAGCCG	60
GGGAAACAAAC GCAGAAACCA CGGTCGGACG	90

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 10T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

ACCCGTGGTC CGTCCGACCG TGGTTTCTGC GTTGTTCGGC CGGCTCGTCC GGCTGAAGAA	60
GCTACCTCCC TGGAAGGTGC TCTGTCCGGC	90

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 11B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

AAACCGGCGG GCACGGGTG TCCCACGGAC GCGGCGGACG GGAGGTGGAC GGCGGACCAG	60
CGTGGTGCTG ACGACCAACG GACGGGTGGG	90

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 11T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

ACCCGTCACT CCCACCCGTC CGTTGGTCGT CAGCACCAACG CTGGTCCGCC GTCCACCTCC	60
CGTCCGCCGC GTCCGTGGGA CACCCCGTGC	90

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 12B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

TCAGGGACGG ACGCAGGGAG GACAGCAGGA AGGACGGACG CAGCTGTTCT TTGTCACCGG	60
AGGAGTACAG GAAGTGTGTTG GTTTCAGCGT	90

(2) INFORMATION FOR SEQ ID NO:666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 12T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

CCGCCGGTTT ACGCTGAAAC CAAACACTTC CTGTACTCCT CCGGTGACAA AGAACAGCTG	60
CGTCCGTCCT TCCTGCTGTC CTCCCCTGGGT	90

(2) INFORMATION FOR SEQ ID NO:667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 13B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

GCTGGGGCAG ACGGGCAGA CGACGGGGGG TGCCCCGCAT CCACGGACGG GAAACCCAGGA	60
AGATAGTTTC AACCAGACGA CGAGCACCGG	90

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 13T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

CCGTCCCTGA CCGGTGCTCG TCGTCTGGTT GAAACTATCT TCCTGGGTTTC CCGTCCGTGG	60
ATGCCGGGCA CCCCGCGTCG TCTGCCGCGT	90

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 14B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

GCGGGCAGTG GGTTTCAGC AGAACACCAT ACGGGCACTG AGCGTGGTTG CCCAGCAGTT	60
CCAGGAACAG CGGACGCATC TGCCAGTAAC	90

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 14T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

CTGCCGCAGC GTTACTGGCA GATGCGTCCG CTGTTCTGG AACTGCTGGG CAACCACGCT	60
CAGTGCCCGT ATGGTGTCT GCTGAAAACC	90

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 15B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

GGTCGGTATC TTCTTCTTCC GGAGCAGCAA CGGAACCCTG CGGTTTTCA CGAGCGCAA	60
CACCAAGCAGC CGGGGTAAACA GCAGCACGCA	90

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 15T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

CACTGCCCGC TGCCTGCTGC TGTTACCCCCG GCTGCTGGTG TTTGCGCTCG TGAAAAACCG	60
CAGGGTTCCG TTGCTGCTCC GGAAGAAGAA	90

(2) INFORMATION FOR SEQ ID NO:673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 16B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

GCGGAACCAG ACGACGCAGG CATGCACGAA CGAAACCGTA AACCTGCCAC GGGGAGGAGT	60
GCTGACGCAG CAGCTGAACC AGACGACGCG	90

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 16T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

GATACCGACC CGCGTCGTCT GGTTCAAGCTG CTGCGTCAGC ACTCCTCCCC GTGGCAGGTT	60
TACGGTTTCG TTCGTGCATG CCTGCGTCGT	90

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 17B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

GGGACAGTTT AGCGTGTGTTA CCCAGGGAGA TGAATTTTTT GGTGTTACGC AGGAAACGAC	60
GTTCGTTGTC ACGGGAACCC CACAGACCCG	90

(2) INFORMATION FOR SEQ ID NO:676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 17T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

CTGGTTCCGC CGGGTCTGTG GGGTTCCCGT CACAAACGAAC GTCGTTCCCT GCGTAACACC	60
AAAAAAATTCA TCTCCCTGGG TAAACACGCT	90

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 18B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

GGTGTTCAGC AGCCGGAACG CAACCAACAC CCGGAGAACG ACGCAGCCAA GCGCAGTCAC	60
GAACGGACAT TTTCCAGGTC AGTTCCCTGCA	90

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 18T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

AAACTGTCCC TGCAGGAAC GACCTGGAAA ATGTCGTTTC GTGACTGCGC TTGGCTGCGT	60
CGTTCTCCGG GTGTTGGTTG CGTTCCGGCT	90

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 19B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

CGTAAACGTA GAAGAAGGAA CGCAGCAGTT CAACAACGTA TACGGACATC AGCCAGTGCA	60
GGAATTAGC CAGGATTCT TCACGCAGAC	90

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 19T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

GCTAACACC GTCTGCGTGA AGAAATCCTG GCTAAATTCC TGCAGTGGCT GATGTCCGTA	60
TACGTTGTTG AACTGCTGCG TTCCTTCTTC	90

(2) INFORMATION FOR SEQ ID NO:681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 20B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

GTTCAGGTG CTGACGGATA CCGATGGACT GCAGTTGGA CCAAACGGAT TTACGGTAGA	60
AGAACAGACG GTTTTCTGG AAGGTGGTT	90

(2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 20T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

TACGTTACCG AAACCACCTT CCAGAAAAAC CGTCTGTTCT TCTACCGTAA ATCCGTTGG	60
TCCAAACTGC AGTCCATCGG TATCCGTCAG	90

(2) INFORMATION FOR SEQ ID NO:683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..89
- (D) OTHER INFORMATION: /note= "oligonucleotide 21B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

GATGAAACGC AGACGGGAGG TCAGCAGAGC CGGACGAGCT TCACGGTGCT GACGAACCTC	60
AGCTTCGGAC AGTTCACGCA GCTGAACAC	89

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 21T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

CACCTGAAAAC GTGTTCAGCT GCGTGAAC TG TCCGAAGCTG AAGTTCGTCA GCACCGTGAA	60
GCTCGTCCGG CTCTGCTGAC CTCCCGTCTG	90

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 22B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

TCAGACGCTC AGCACGTTT TCACGACGGA AGGTACGAGC ACCAACAAACG TAGTCCATGT	60
TTACGATCGG ACGCAGACCG TCCGGTTTCG	90

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 22T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

CGTTTCATCC CGAAACCGGA CGGTCTGCGT CCGATCGTAA ACATGGACTA CGTTGTTGGT	60
GCTCGTACCT TCCGTCGTGA AAAACGTGCT	90

(2) INFORMATION FOR SEQ ID NO:687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 23B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

CGTCCAGACC CAGAACGGAA GCACCCAGCA GACCCGGACG ACGAGCACGT TCGTAGTTCA	60
GAACGGAGAA CAGAGCTTTA ACACGGGAGG	90

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 23T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

GAGCGTCTGA CCTCCCGTGT TAAAGCTCTG TTCTCCGTTTC TGAACATACGA ACGTGCTCGT	60
CGTCCGGGTC TGCTGGGTGC TTCCGTTCTG	90

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 24B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

CGGTAACGTC AACTTTAACG AAGTACAGTT CCGGCGGCGG GTCCTGAGCA CGAACACGCA	60
GAACGAAGGT ACGCCAAGCA CGGTGGATGT	90

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 24T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

GGTCTGGACG ACATCCACCG TGCTTGGCGT ACCTTCGTTTC TGCCTGTTCG TGCTCAGGAC	60
CCGCCGCCGG AACTGTACTT CGTTAAAGTT	90

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 25B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

CGTAACGACG AACGCAGTAG GTGTTCTGCG GTTTGATGAT GGAAGCGATA ACTTCGGTCA	60
GACGGTCCTG CGGGATGGTG TCGTACGCGC	90

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 25T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

GACGTTACCG GCGCGTACGA CACCATCCCG CAGGACCGTC TGACCGAAGT TATCGCTTCC	60
ATCATCAAAC CGCAGAACAC CTACTGCGTT	90

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 26B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

GACGCATGTA CGGCTGCAGG TCGGTCAAGG TGAAACGTG GGATTGAAT GCTTACGAA	60
CGTGACCGTG AGCAGCTTC TGAACAACAG	90

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 26T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

CGTCGTTACG CTGTTGTTCA GAAAGCTGCT CACGGTCACG TTCTAAAGC ATTCAAATCC	60
CACGTTTCCA CCCTGACCGA CCTGCAGCCG	90

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 27B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

GACCGGAGGA AGCTTCGTTCA AGGGAGGAGG ACTGTTGAT AACAACAGCG TCACGCAGCG	60
GGGAGGTTTC CTGCAGGTGA GCAACGAAC	90

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 27T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

TACATGCGTC AGTTCGTTGC TCACCTGCAG GAAACCTCCC CGCTGCGTGA CGCTGTTGTT	60
ATCGAACAGT CCTCCTCCCT GAACGAAAGCT	90

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 28B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

AACCCTGCGG GATAACCCTGG CACTGAACGT AGGATTACCC AC GGATAACGA ACAGCGTGGT	60
GGCACATGAA ACGCAGGAAA ACGTCGAACA	90

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 28T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

TCCTCCGGTC TGTCGACGT TTTCCTGCGT TTCATGTGCC ACCACGCTGT TCGTATCCGT	60
GGTAAATCCT ACGTTCAGTG CCAGGGTATC	90

(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 29B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

GCAGCAGCAG ACCGTCACGA CGGATACCAG CGAACAGTTT GTTTCCATG TCACCGTAGC	60
ACAGGGAGCA CAGCAGGGTG GACAGGATGG	90

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 29T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

CCGCAGGGTT CCATCCTGTC CACCCTGCTG TGCTCCCTGT GCTACGGTGA CATGGAAAAC	60
AAACTGTTCG CTGGTATCCG TCGTGACGGT	90

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 30B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

CGTATTCCGG AACACCACGA ACCAGGGTAC GCAGGAAGGT TTTAGCGTGG GTCAGGTGCG	60
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GAGTAACCAG CAGGAAGTCG TCAACCAGAC	90
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(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 30T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

CTGCTGCTGC GTCTGGTTGA CGACTTCCTG CTGGTTACTC CGCACCTGAC CCACGCTAAA	60
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ACCTTCCTGC GTACCCTGGT TCGTGGTGTT	90
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(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 31B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

GAGCCGGCAT CTGAACGAAA GCGGTGCCAC CCAGAGCTTC GTCTTCAACC GGGAAAGTTAA	60
CAACGGTTTT ACGCAGGTTT ACAACGCAAC	90

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 31T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

CCGGAATAACG GTTGCCTTGT AAACCTGCGT AAAACCGTTG TTAACCTCCC GGTTGAAGAC	60
GAAGCTCTGG GTGGCACCGC TTTCGTTCAAG	90

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 32B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

GGATGGAGGT ACGAGCGTAG GAGGAGTAGT CGGACTGAAC TTCCAGGGTA CGGGTGTCCA	60
GCAGCAGACC GCACCACGGG AACAGACCGT	90

(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 32T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

ATGCCGGCTC ACGGTCTGTT CCCGTGGTGC GGTCTGCTGC TGGACACCCG TACCCTGGAA	60
GTCAGTCCG ACTACTCCTC CTACGCTCGT	90

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 33B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

GGGAGTGGCA TTTCAGACGC AGAACACCGA ACAGTTACG ACGCATGTTA CGACCAGCTT	60
TGAAACCACG GTTGAAGGTC AGGGAAGCAC	90

(2) INFORMATION FOR SEQ ID NO:708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 33T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

ACCTCCATCC GTGCTTCCCT GACCTTCAAC CGTGGTTCA AAGCTGGTCG TAACATGCGT	60
CGTAAACTGT TCGGTGTTCT GCGTCTGAAA	90

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 34B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

ACCCGTGGAA ACGGTAAGCC TGCAGCAGCA GGATTGGTGA GATGTTGGTG CAAACGGTCT	60
GCAGGGAGTT TACCTGCAGG TCCAGGAACA	90

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 34T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

TGCCACTCCC TGTTCCCTGGA CCTGCAGGTA AACTCCCTGC AGACCCTTG CACCAACATC	60
TACAAAATCC TGCTGCTGCA GGCTTACCGT	90

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 35B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

AGTAGCACAG GGAAGCGGTG TCGGAGATAA CACCCAGGAA GAAGGTCGGG TTTTCCAAA	60
CCTGCTGGTG GAACGGCAGC TGCAGAACGC	90

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 35T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

TTCCACGCGT GCGTTCTGCA GCTGCCGTTC CACCAGCAGG TTTGGAAAAA CCCGACCTTC	60
TTCCTGCGTG TTATCTCCGA CACCGCTTCC	90

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 36B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

GGCACAGCCA CTGAACAGCT TCGGACGGCA GCGGACCAGC AGCACCTTA GCACCCAGGG	60
ACATACCAGC GTTTTAGCT TTCAGGATGG	90

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 36T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

CTGTGCTACT CCATCCTGAA AGCTAAAAAC GCTGGTATGT CCCTGGGTGC TAAAGGTGCT	60
GCTGGTCCGC TGCCGTCCGA AGCTGTTCA	90

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: /note= "oligonucleotide 37B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

ACAGCTGGGT CTGAGCGGTA CGCAGGGAAC CCAGCAGCGG AACGTAGGTA ACACGGTGAC	60
GGGTCAAGTTT CAGCAGGAAA GCCTGGT	87

(2) INFORMATION FOR SEQ ID NO:716:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: /note= "oligonucleotide 37T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

TGGCTGTGCC ACCAGGCTTT CCTGCTGAAA CTGACCCGTC ACCGTGTTAC CTACGTTCCG	60
CTGCTGGGTT CCCTGCGTAC CGCTCAG	87

(2) INFORMATION FOR SEQ ID NO:717:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: /note= "oligonucleotide 38B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

ACGGCAGAGC CGGGTTAGCA GCAGCTTCCA GAGCGGTCAG GGTGGTACCC GGCAGTTAC	60
GGG	63

(2) INFORMATION FOR SEQ ID NO:718:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: /note= "oligonucleotide 38T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

ACCCAGCTGT CCCGTAAACT GCCGGGTACC ACCCTGACCG CTCTGGAAGC TGCTGCTAAC	60
CCGG	64

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: /note= "oligonucleotide 39B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

GGTGCCCTCG AGGAATTCTGG ATCCATTAGT CCAGGATGGT TTTGAAGTCG	50
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(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: /note= "oligonucleotide 39T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

CTCTGCCGTC CGACTTCAAA ACCATCCTGG ACTAATGGAT CCGAATTCT CGAGGCACGC	60
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(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3451
- (D) OTHER INFORMATION: /note= "hTRT sequence employing codon distribution preferentially used by highly expressed genes in E. coli containing SacI and XhoI sites"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

GCACCGGGGA GCTCTAGAGT CGACCATATG CCGCGTGCTC CGCGTTGCCG TGCTGTTCGT	60
TCCCTGCTGC GTTCCCACTA TCGCGAAGTT CTGCCGCTGG CTACCTTCGT TCGTCGTCTG	120
GGCCCGCAGG GTTGGCGTCT GGTTCAAGCT GGTGACCCGG CTGCTTCCG TGCTCTGGTT	180
GCTCAGTGCC TGGTTTGCCT TCCGTGGGAC GCTCGTCCGC CGCCGGCTGC TCCGTCCCTC	240
CGTCAGGTTT CCTGCCTGAA AGAACTGGTT GCTCGTGTTC TGCAGCGTCT GTGCGAACGT	300
GGTGCTAAAA ACGTTCTGGC TTTCGGTTTC GCTCTGCTGG ACGGTGCTCG TGGTGGTCCG	360
CCGGAAGCAT TCACCAACCTC CGTCGTTCC TACCTGCCGA ACACCGTTAC CGACCGCTCTG	420
CGTGGTTCCG GTGCTTGGGG TCTGCTGCTG CGTCGTGTTG GTGACGACGT TCTGGTTCAC	480
CTGCTGGCTC GTTGCCTCT GTTCGTTCTG GTTGCTCCGT CCTGCGCTTA CCAGGTTTGT	540
GSTCCGCCGC TGTACCAGCT GGGTGCTGCT ACCCAGGCTC GTCCGCCGCC GCACGCTTCC	600
GGTCCCGCTC GTCGTCTGGG TTGCGAACGT GCTTGAACC ACTCCGTTCG TGAAGCTGGT	660
GTTCGGCTGG GTCTGCCGGC TCCGGGTGCT CGTCGTGCTG GTGGTTCCGC TTCCCGTTCC	720
CTGCCGCTGC CGAAACGTCC GCGTCGTGGT GCTGCTCCGG AACCGGAACG TACCCCGTT	780
GGTCAGGGTT CCTGGGCTCA CCCGGGTGCT ACCCGTGGTC CGTCCGACCG TGGTTCTGC	840
GTTGTTCCC CGGCTCGTCC GGCTGAAGAA GCTACCTCCC TGGAAAGGTGC TCTGTCCGGC	900
ACCCGTCACT CCCACCCGTC CGTTGGTCGT CAGCACCACG CTGGTCCGCC GTCCACCTCC	960
CGTCCGCCGC GTCCGTGGGA CACCCCGTGC CGGCCGGTT ACGCTGAAAC CAAACACTTC	1020
CTGTACTCCT CCGGTGACAA AGAACAGCTG CGTCGGCTCT TCCTGCTGTC CTCCCTGCGT	1080
CCGTCCCTGA CCGGTGCTCG TCGTCTGGTT GAAACTATCT TCCTGGGTTC CCGTCCGTGG	1140
ATGCCGGGCA CCCCGCGTCG TCTGCCGCGT CTGCCGCAGC GTTACTGGCA GATGCGTCCG	1200

CTGTTCTGG AACTGCTGGG CAACCACGCT CAGTGCCGT ATGGTGTCT GCTGAAAACC	1260
CACTGCCCGC TGCCTGCTGC TGTTACCCCG GCTGCTGGTG TTTGCCTCG TGAAAAACCG	1320
CAGGGTTCCCG TTGCTGCTCC GGAAGAAGAA GATACCGACC CGCGTCGTCT GGTCAGCTG	1380
CTGCGTCAGC ACTCCCTCCCC GTGGCAGGTT TACGGTTTCG TTCGTGCATG CCTGCCTCGT	1440
CTGGTTCCCG CGGGTCTGTG GGGTTCCCGT CACAACGAAC GTCGTTCCCT GCGTAACACC	1500
AAAAAAATTCA TCTCCCTGGG TAAACACGCT AAACTGTCCC TGCAGGAAC GACCTGGAAA	1560
ATGTCCGTTG GTGACTGCGC TTGGCTGCGT CGTTCTCCGG GTGTTGGTTG CGTTCCGGCT	1620
GCTGAACACC GTCTGCGTGA AGAAATCCTG GCTAAATTCC TGCACTGGCT GATGTCCGTA	1680
TACGTTGTTG AACTGCTGCG TTCCCTCTTC TACGTTACCG AAACCACCTT CCAGAAAAAC	1740
CGTCTGTTCT TCTACCGTAA ATCCGTTGG TCCAAACTGC AGTCCATCGG TATCCGTCAG	1800
CACCTGAAAC GTGTTCAGCT GCGTGAACGT TCCGAAGCTG AAGTTCGTCA GCACCGTGAA	1860
GCTCGTCCGG CTCTGCTGAC CTCCCGTCTG CGTTCATCC CGAAACCGGA CGGTCTGCGT	1920
CCGATCGTAA ACATGGACTA CGTTGTTGGT GCTCGTACCT TCCGTCGTGA AAAACGTGCT	1980
GACCGTCTGA CCTCCCGTGT TAAAGCTCTG TTCTCCGTT TGAACACTACGA ACGTGCTCGT	2040
CGTCCGGGTC TGCTGGGTGC TTCCGTTCTG GGTCTGGACG ACATCCACCG TGCTGGCGT	2100
ACCTTCGTTG TGCGTGTTCG TGCTCAGGAC CCGCCGCCGG AACTGTACTT CGTTAAAGTT	2160
GACGTTACCG GCGCGTACGA CACCATCCCC CAGGACCGTC TGACCGAAGT TATCGCTTCC	2220
ATCATCAAAC CGCAGAACAC CTACTGCGTT CGTCGTTACG CTGTTGTTCA GAAAGCTGCT	2280
CACCGTCACG TTCTAAAGC ATTCAAATCC CACGTTCCA CCCTGACCGA CCTGCAGCCG	2340
TACATGCGTC AGTCGTTGC TCACCTGCAG GAAACCTCCC CGCTGCGTGA CGCTGTTGTT	2400
ATCGAACAGT CCTCCTCCCT GAACGAAGCT TCCTCCGGTC TGTCGACGT TTTCCTGCGT	2460
TTCATGTGCC ACCACGCTGT TCGTATCCGT GGTAAATCCT ACGTTCAGTG CCAGGGTATC	2520
CCGCAGGGTT CCATCCTGTC CACCCGTCTG TGCTCCCTGT GCTACGGTGA CATGGAAAAC	2580
AAACTGTTCG CTGGTATCCG TCGTGACGGT CTGCTGCTGC GTCTGGTTGA CGACTTCCTG	2640
CTGGTTACTC CGCACCTGAC CCACGCTAAA ACCTTCCTGC GTACCCCTGGT TCGTGGTGTT	2700
CCGGAATAACG GTTGCCTGTT AACACCTGCGT AAAACCGTTG TTAACCTCCC GGTTGAAGAC	2760
GAAGCTCTGG GTGGCACCGC TTTCGTTCAAG ATGCCGGCTC ACGGTCTGTT CCCGTGGTGC	2820
GGCTGCTGC TGGACACCCG TACCCCTGGAA GTTCAGTCCG ACTACTCCTC CTACGCTCGT	2880
ACCTCCATCC GTGCTTCCCT GACCTTCAAC CGTGGTTCA AAGCTGGTCG TAACATGCGT	2940
CGTAAACTGT TCGGTGTTCT GCGTCTGAAA TGCCACTCCC TGTTCTGGA CCTGCAGGTA	3000
AACTCCCTGC AGACCGTTG CACCAACATC TACAAAATCC TGCTGCTGCA GGCTTACCGT	3060

TTCCACGCGT GCGTTCTGCA GCTGCCGTT CACCAGCAGG TTTGGAAAAA CCCGACCTTC	3120
TTCCCTGCGTG TTATCTCCGA CACCGCTTCC CTGTGCTACT CCATCCTGAA AGCTAAAAAC	3180
GCTGGTATGT CCCTGGGTGC TAAAGGTGCT GCTGGTCCGC TGCCGTCCGA AGCTGTTCAG	3240
TGGCTGTGCC ACCAGGCTTT CCTGCTGAAA CTGACCCGTC ACCGTGTTAC CTACGTTCCG	3300
CTGCTGGTT CCCTGCGTAC CGCTCAGACC CAGCTGTCCC GTAAACTGCC GGGTACCACC	3360
CTGACCGCTC TGGAAGCTGC TGCTAACCCG GCTCTGCCGT CCGACTTCAA AACCATCCTG	3420
GACTAATGGA TCCGAATTCC TCGAGGCACG C	3451

(2) INFORMATION FOR SEQ ID NO:722:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..30
 - (D) OTHER INFORMATION: /note= "antisense oligonucleotide corresponding to positions 31-60 of hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

GGCATCGCGG GGGTGGCCGG GGCCAGGGCT	30
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(2) INFORMATION FOR SEQ ID NO:723:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..30
 - (D) OTHER INFORMATION: /note= "antisense oligonucleotide corresponding to positions 496-525 of hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

GCGCAGCGTG CCAGCAGGTG AACCAAGCACG	30
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(2) INFORMATION FOR SEQ ID NO:724:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..30
(D) OTHER INFORMATION: /note= "antisense oligonucleotide corresponding to positions 631-660 of hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

GCCCCGTTCCGC ATCCCAGACG CCTTCGGGGT

30

(2) INFORMATION FOR SEQ ID NO:725:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..30
(D) OTHER INFORMATION: /note= "antisense oligonucleotide corresponding to positions 646-675 of hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

ACGCTATGGT TCCAGGCCCG TTCGCATCCC

30

(2) INFORMATION FOR SEQ ID NO:726:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: /note= "sequence present in pGRN176 but not pGRN175"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

GTGGCGGAGG GACTGGGGAC CCGGGCACCG GTCCTGCCCC TTCACCTTCC AGCTCCGCCT	60
CGTCCGCGCG GAACCCCGCC CCGTCCCGAA CCCTTCCCGG GTCCCCGGCC CAGCCCCCTTC	120
CGGG	124

(2) INFORMATION FOR SEQ ID NO:727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..300
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa at positions 1-300 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 630
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa at position 630 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 649..663
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa at positions 649-663 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 674..688
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa at positions 674-688 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 701..706
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa at positions 701-706 may be present or absent"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 771..790
(D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa at positions 771-790 may be
 present or absent"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 887..937
(D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa at positions 887-937 may be
 present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 965..994
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 965-994 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1018..1027
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 1018-1027 may
be present or absent"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

Xaa		
485	490	495
Xaa		
500	505	510
Xaa		
515	520	525
Xaa		
530	535	540
Xaa		
545	550	555
Xaa		
565	570	575
Xaa		
580	585	590
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa		
595	600	605
Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa		
610	615	620
Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa		
625	630	635
Xaa Xaa Ile Xaa		
645	650	655
Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Val Xaa Xaa Xaa Xaa Xaa		
660	665	670
Xaa		
675	680	685
Xaa Xaa Xaa Arg Xaa Xaa Pro Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa		
690	695	700
Xaa Xaa Arg Xaa Ile Xaa		
705	710	715
Xaa		
725	730	735
Xaa		
740	745	750
Xaa		
755	760	765
Xaa		
770	775	780
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Asp Xaa		
785	790	795
800		

Xaa
865 870 875 880

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Gly Xaa
 930 935 940

Xaa Gln Gly Xaa Xaa Xaa Ser Xaa Xaa

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Asp Xaa Leu Xaa Xaa Xaa Xaa

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